

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 108 Seconds  
(without alignments)  
564.248 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVLVQSGAEVKKPGASVKV.....YDYVYGMVDWVGQGTIVTWS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*
- 11: Geneseqp2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	672	100.0	125	7	ADK18776	Adk18776	Anti-huma
2	672	100.0	125	7	ADK18948	Adk18948	Anti-huma
3	672	100.0	125	7	ADK18624	Adk18624	Anti-huma
4	672	100.0	125	7	ADK18813	Adk18813	Anti-huma
5	672	100.0	125	8	ADL25392	Human mAb	Adl25392
6	638	94.9	125	7	ADK18614	Adk18614	Anti-huma
7	638	94.9	125	7	ADK18779	Adk18779	Anti-huma
8	638	94.9	125	7	ADK18919	Adk18919	Anti-huma
9	638	94.9	125	7	ADK18816	Adk18816	Anti-huma
10	638	94.9	125	8	ADL25444	Human mAb	Adl25444
11	593.5	88.3	126	7	ADK18864	Adk18864	Anti-huma
12	593.5	88.3	126	7	ADK18595	Adk18595	Anti-huma
13	593.5	88.3	126	7	ADK18777	Adk18777	Anti-huma
14	593.5	88.3	126	8	ADL25408	Human mAb	Adl25408
15	588	87.5	123	10	AEK98538	Human ant	Aek98538
16	579.5	86.2	125	7	ADK18814	Adk18814	Anti-huma
17	578	86.0	119	10	AEH94456	Anti-ten-	Aeh94456
18	575.5	85.6	126	7	ADK18925	Adk18925	Anti-huma
19	575.5	85.6	126	7	ADK18780	Adk18780	Anti-huma
20	575.5	85.6	126	7	ADK18616	Adk18616	Anti-huma
21	575.5	85.6	126	7	ADK18817	Adk18817	Anti-huma
22	575.5	85.6	126	8	ADL25448	Human mAb	Adl25448

23	572	85.1	127	7	ADK18620	Adk18620 Anti-huma
24	572	85.1	127	7	ADK18818	Adk18818 Anti-huma
25	572	85.1	127	7	ADK18781	Adk18781 Anti-huma
26	572	85.1	127	7	ADK18936	Adk18936 Anti-huma
27	572	85.1	127	8	ADL25456	Adl25456 Human mAb
28	571	85.0	123	10	AEK98534	Aek98534 Human ant
29	570	84.8	126	10	AEI64964	Aei64964 Anti-Ang-
30	570	84.8	126	10	AEI64968	Aei64968 Anti-Ang-
31	567.5	84.4	126	7	ADK18597	Adk18597 Anti-huma
32	567.5	84.4	126	7	ADK18870	Adk18870 Anti-huma
33	567.5	84.4	126	7	ADK18812	Adk18812 Anti-huma
34	567.5	84.4	126	7	ADK18775	Adk18775 Anti-huma
35	567.5	84.4	126	8	ADL25412	Adl25412 Human mAb
36	566	84.2	127	10	AEJ20382	Aej20382 Anti-IRTA
37	564.5	84.0	124	10	AEI14838	Aei14838 Human ant
38	563.5	83.9	124	10	AEI14842	Aei14842 Human ant
39	561.5	83.6	122	6	ABR55829	Abr55829 Heavy cha
40	561.5	83.6	122	10	AEI17553	Aei17553 Human ang
41	561.5	83.6	126	7	ADK18778	Adk18778 Anti-huma
42	561.5	83.6	126	7	ADK18613	Adk18613 Anti-huma
43	561.5	83.6	126	7	ADK18815	Adk18815 Anti-huma
44	561.5	83.6	126	8	ADL25464	Adl25464 Human mAb
45	558.5	83.1	121	10	AEI65125	Aei65125 Anti-Ang-

ALIGNMENTS

RESULT 1  
ADK18776  
ID ADK18776 standard; protein; 125 AA.  
AC ADK18776;  
XX  
DT 06-MAY-2004 (first entry)  
DE  
DE 'Anti-human PDGF-D antibody protein related sequence #2.  
XX  
KW antinflammatory; immunomodulator; cytostatic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057857-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 06-JAN-2003; 2003WO-US000398.  
XX  
PR 07-JAN-2002; 2002US-00041860.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
XX Bezabeh B;  
XX WPI; 2003-587119/55.  
XX  
XX New human monoclonal antibody that binds to platelet-derived growth  
XX factor-D (PDGF-D), useful for treating chronic and recurrent human  
XX diseases, such as inflammation, autoimmunity and cancer.  
XX  
XX Disclosure; SEQ ID NO 200; 255pp; English.

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained from HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

XX SQ Sequence 125 AA;

Query Match 100.0%; Score 672; DB 7; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-54;  
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120  
 DB 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120

QY 121 VTVSS 125  
 DB 121 VTVSS 125

RESULT 2  
 ADK18948  
 ID ADK18948 standard; protein; 125 AA.  
 AC ADK18948;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Anti-human PDGF-D antibody protein related sequence #174.  
 XX  
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057857-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 06-JAN-2003; 2003WO-US000398.  
 XX  
 PR 07-JAN-2002; 2002US-00041860.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Corvalan JRF; Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX  
 DR WPI; 2003-587119/55.  
 XX  
 XX New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 XX  
 PS Disclosure; SEQ ID NO 372; 255pp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody that binds to  
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.

XX SQ Sequence 125 AA;

Query Match 100.0%; Score 672; DB 7; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-54;  
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120  
 DB 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120

QY 121 VTVSS 125  
 DB 121 VTVSS 125

RESULT 3  
 ADK18624  
 ID ADK18624 standard; protein; 125 AA.  
 XX  
 AC ADK18624;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Anti-human PDGF-D antibody heavy chain protein sequence.  
 XX  
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057857-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 06-JAN-2003; 2003WO-US000398.  
 XX  
 PR 07-JAN-2002; 2002US-00041860.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Corvalan JRF; Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX  
 DR WPI; 2003-587119/55.  
 XX  
 XX New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 XX  
 PS Disclosure; SEQ ID NO 48; 255pp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody that binds to  
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.

XX SQ Sequence 125 AA;

Query Match 100.0%; Score 672; DB 7; Length 125;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-54;  
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120  
 DB 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120

QY 121 VTVSS 125

```

Db      121 VTVSS 125
|||||
RESULT 4
ADK18813
ID   ADK18813 standard; protein; 125 AA.
XX
AC   ADK18813;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Anti-human PDGF-D antibody protein related sequence #39.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003057857-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 237; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 30664188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 125 AA;

Query Match      100.0%; Score 672; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY   61 AQKFGQVRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYVYGMVWGQGT 120
DB   61 AQKFGQVRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYVYGMVWGQGT 120

QY   121 VTVSS 125
DB   121 VTVSS 125

RESULT 5
ADL25392
ID   ADL25392 standard; protein; 125 AA.
XX
AC   ADL25392;
XX
DT   17-JUN-2004 (first entry)
XX
DE   Human mab 6.4 heavy chain variable region protein SEQ ID NO:2.
XX
KW   antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW   nephritis; mesangial cell proliferation inhibition;
KW   mesangial proliferative glomerulonephritis; nephrotropic;
KW   antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW   gene therapy; human; monoclonal antibody; mAb.
XX
OS   Homo sapiens.
XX
PN   WO2004024098-A2.
XX
PD   25-MAR-2004.
XX
PF   16-SEP-2003; 2003WO-US029414.
XX
PR   16-SEP-2002; 2002US-0411137P.
XX
PA   (ABGE-) ABGENIX INC.
PA   (CURA-) CURAGEN CORP.
XX
PI   Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;
PI   WPI; 2004-269881/25.
DR   N-PSDB; ADL25391.
XX
PT   Use of an antibody or its binding fragment that binds platelet derived
PT   growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT   nephritis.
XX
PS   Disclosure; SEQ ID NO 2; 115pp; English.
XX
CC   The present invention describes an antibody or its binding fragment that
CC   binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC   useful in preparing a medicament for treating nephritis. Also described:
CC   (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC   (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC   of treating mesangial proliferative glomerulonephritis. The antibody has
CC   nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC   antidiabetic activities, and can be used in gene therapy. The antibody or
CC   its binding fragment, that binds PDGF-DD, can be used in preparing a
CC   medicament for treating nephritis and related disorders, e.g., mesangial
CC   proliferative glomerulonephritis. The present sequence represents a human
CC   monoclonal antibody (mAb) variable region sequence, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 125 AA;

Query Match      100.0%; Score 672; DB 8; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY   61 AQKFGQVRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYVYGMVWGQGT 120
DB   61 AQKFGQVRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYVYGMVWGQGT 120

QY   121 VTVSS 125
DB   121 VTVSS 125

RESULT 6
ADK18614
ID   ADK18614 standard; protein; 125 AA.
XX

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AC ADK18614;
XX
XX 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody heavy chain protein sequence.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 38; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 125 AA;
XX
XX Query Match 94.9%; Score 638; DB 7; Length 125;
XX Best Local Similarity 94.4%; Pred. No. 4.7e-51;
XX Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60
QY 61 AQKFGQRTVMTSDTSISTAYMELSSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
Db 61 AQKFGQRTVMTSDTSISTAYMELSSLRSEDTAVYYCARGSGSYGYDYGGMDVWGQGT 120
QY 121 VTVSS 125
Db 121 VTVSS 125
XX
XX RESULT 7
XX ADK18779
XX ID ADK18779 standard; protein; 125 AA.
XX
XX AC ADK18779;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #5.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX
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OS Homo sapiens.
XX
XX WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 203; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 125 AA;
XX
XX Query Match 94.9%; Score 638; DB 7; Length 125;
XX Best Local Similarity 94.4%; Pred. No. 4.7e-51;
XX Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60
QY 61 AQKFGQRTVMTSDTSISTAYMELSSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
Db 61 AQKFGQRTVMTSDTSISTAYMELSSLRSEDTAVYYCARGSGSYGYDYGGMDVWGQGT 120
QY 121 VTVSS 125
Db 121 VTVSS 125
XX
XX RESULT 8
XX ADK18919
XX ID ADK18919 standard; protein; 125 AA.
XX
XX AC ADK18919;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #145.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX
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PR 07-JAN-2002; 2002US-00041860.  
XX (ABGE-) ABGENIX INC.  
PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
XX Bezabeh B;  
XX WPI; 2003-587119/55.  
XX  
XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX  
XX Disclosure; SEQ ID NO 343; 255pp; English.  
XX  
XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX  
SQ Sequence 125 AA;  
Query Match 94.9%; Score 638; DB 7; Length 125;  
Best Local Similarity 94.4%; Pred. No. 4.7e-51;  
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60  
QY 61 AQKFGQRTVMTRTDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120  
DB 61 AQKFGQRTVMTRTDTSISTAYMELSSLRSEDTAVYYCARGSGYSYGYDYYGMDVWGQGT 120  
QY 121 VTSS 125  
DB 121 VTSS 125  
RESULT 9  
ADK18816  
ID ADK18816 standard; protein; 125 AA.  
XX  
AC ADK18816;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Anti-human PDGF-D antibody protein related sequence #42.  
XX  
KW antinflammatory; immunomodulator; cytostatic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057857-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 06-JAN-2003; 2003WO-US000398.  
XX  
PR 07-JAN-2002; 2002US-00041860.  
XX  
XX (ABGE-) ABGENIX INC.  
PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX WPI; 2003-587119/55.  
XX  
XX Use of an antibody or its binding fragment that binds platelet derived  
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating

XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX  
XX Disclosure; SEQ ID NO 240; 255pp; English.  
XX  
XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX  
SQ Sequence 125 AA;  
Query Match 94.9%; Score 638; DB 7; Length 125;  
Best Local Similarity 94.4%; Pred. No. 4.7e-51;  
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60  
QY 61 AQKFGQRTVMTRTDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120  
DB 61 AQKFGQRTVMTRTDTSISTAYMELSSLRSEDTAVYYCARGSGYSYGYDYYGMDVWGQGT 120  
QY 121 VTSS 125  
DB 121 VTSS 125  
RESULT 10  
ADL25444  
ID ADL25444 standard; protein; 125 AA.  
XX  
AC ADL25444;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human mAb 1.45 heavy chain variable region protein SEQ ID NO:54.  
XX  
KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;  
KW nephritis; mesangial cell proliferation inhibition;  
KW mesangial proliferative glomerulonephritis; nephrotropic;  
KW antinflammatory; dermatological; immunosuppressive; antidiabetic;  
KW gene therapy; human; monoclonal antibody; mAb.  
XX  
OS Homo sapiens.  
XX  
PN WO2004024098-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 16-SEP-2003; 2003WO-US029414.  
XX  
PR 16-SEP-2002; 2002US-0411137P.  
XX  
XX (ABGE-) ABGENIX INC.  
PA (CURA-) CURAGEN CORP.  
XX  
PI Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;  
XX WPI; 2004-269881/25.  
DR N-PSDB; ADL25443.  
XX  
PT Use of an antibody or its binding fragment that binds platelet derived  
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating

PT nephritis.  
 PS Disclosure; SEQ ID NO 54; 115pp; English.  
 XX  
 CC The present invention describes an antibody or its binding fragment that  
 CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is  
 CC useful in preparing a medicament for treating nephritis. Also described:  
 CC (1) a method of detecting nephritis; (2) a method of treating nephritis;  
 CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method  
 CC of treating mesangial proliferative glomerulonephritis. The antibody has  
 CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and  
 CC antidiabetic activities, and can be used in gene therapy. The antibody or  
 CC its binding fragment, that binds PDGF-DD, can be used in preparing a  
 CC medicament for treating nephritis and related disorders, e.g., mesangial  
 CC proliferative glomerulonephritis. The present sequence represents a human  
 CC monoclonal antibody (mAb) variable region sequence, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 125 AA;  
 Query Match 94.9%; Score 638; DB 8; Length 125;  
 Best Local Similarity 94.4%; Pred. No. 4.7e-51;  
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTDY 60  
 DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60  
 QY 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120  
 DB 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120  
 QY 121 VTVSS 125  
 DB 121 VTVSS 125  
 RESULT 11  
 ADK18864  
 ID ADK18864 standard; protein; 126 AA.  
 AC ADK18864;  
 DT 06-MAY-2004 (first entry)  
 XX Anti-human PDGF-D antibody protein related sequence #90.  
 XX antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 KW Homo sapiens.  
 OS  
 XX WO2003057857-A2.  
 FN 17-JUL-2003.  
 PD 06-JAN-2003; 2003WO-US000398.  
 XX 07-JAN-2002; 2002US-00041860.  
 PR (ABGE-) ABGENIX INC.  
 PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX WPI; 2003-587119/55.  
 DR New human monoclonal antibody that binds to platelet-derived growth  
 XX factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 PT  
 XX Disclosure; SEQ ID NO 288; 255pp; English.  
 PS The invention relates to a human monoclonal antibody that binds to  
 XX

CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.  
 XX  
 SQ Sequence 126 AA;  
 Query Match 88.3%; Score 593.5; DB 7; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 6.1e-47;  
 Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;  
 QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTDY 60  
 DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60  
 QY 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119  
 DB 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCAREGIAVAGTYYYGMDVWGQGT 120  
 QY 120 TVTVSS 125  
 DB 121 TVTVSS 126  
 RESULT 12  
 ADK18595  
 ID ADK18595 standard; protein; 126 AA.  
 AC ADK18595;  
 DT 06-MAY-2004 (first entry)  
 XX Anti-human PDGF-D antibody heavy chain protein sequence.  
 XX antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 KW Homo sapiens.  
 OS  
 XX WO2003057857-A2.  
 FN 17-JUL-2003.  
 PD 06-JAN-2003; 2003WO-US000398.  
 XX 07-JAN-2002; 2002US-00041860.  
 PR (ABGE-) ABGENIX INC.  
 PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX WPI; 2003-587119/55.  
 DR New human monoclonal antibody that binds to platelet-derived growth  
 XX factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 PT  
 XX Disclosure; SEQ ID NO 19; 255pp; English.  
 PS The invention relates to a human monoclonal antibody that binds to  
 XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This

CC sequence corresponds to a protein used in the invention.

XX Sequence 126 AA;

Query Match 88.3%; Score 593.5; DB 7; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 6.1e-47;  
 Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQGVMTTRDTSTISYAMELSSLSRSEDYAIYCYVR-GFGYSYNYDYGGMDVWGQGT 119

DB 61 AQKFGQGVMTTRDTSTISYAMELSSLSRSEDYAIYCYVR-GFGYSYNYDYGGMDVWGQGT 120

QY 120 TTVTVSS 125

DB 121 TTVTVSS 126

RESULT 13

ADK18777  
 ID ADK18777 standard; protein; 126 AA.

XX AC ADK18777;

DT 06-MAY-2004 (first entry)

DE Anti-human PDGF-D antibody protein related sequence #3.  
 XX antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 OS Homo sapiens.

XX WO2003057857-A2.

PN 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 DR WPI; 2003-587119/55.  
 XX New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

XX Disclosure; SEQ ID NO 201; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

XX Sequence 126 AA;

Query Match 88.3%; Score 593.5; DB 7; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 6.1e-47;  
 Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQGVMTTRDTSTISYAMELSSLSRSEDYAIYCYVR-GFGYSYNYDYGGMDVWGQGT 119

DB 61 AQKFGQGVMTTRDTSTISYAMELSSLSRSEDYAIYCYVR-GFGYSYNYDYGGMDVWGQGT 120

QY 120 TTVTVSS 125

DB 121 TTVTVSS 126

RESULT 14

ADL25408  
 ID ADL25408 standard; protein; 126 AA.

XX AC ADL25408;

DT 17-JUN-2004 (first entry)

DE Human mAb 1.18 heavy chain variable region protein SEQ ID NO:18.  
 XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;  
 KW nephritis; mesangial cell proliferation inhibition;  
 KW mesangial proliferative glomerulonephritis; nephrotropic;  
 KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;  
 KW gene therapy; human; monoclonal antibody; mAb.

XX Homo sapiens.

XX WO2004024098-A2.

XX 25-MAR-2004.

XX 16-SEP-2003; 2003WO-US029414.

XX 16-SEP-2002; 2002US-0411137P.

XX (ABGE-) ABGENIX INC.

XX (CURA-) CURAGEN CORP.

XX Floege J, Gazit-Bornstein G, Keyt B, Larochelle WJ, Lichenstein H;  
 DR WPI; 2004-269881/25.  
 XX N-PSDB; ADL25407.  
 XX Use of an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD) for preparing a medicament for treating nephritis.

XX Disclosure; SEQ ID NO 18; 115pp; English.

XX The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antiinflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mAb) variable region sequence, which is used in the exemplification of the present invention.

XX Sequence 126 AA;

Query Match 88.3%; Score 593.5; DB 8; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 6.1e-47;  
 Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVQRATQGGLEWGMWNPNSGNTDY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVQRATQGGLEWGMWNPNSGNTGY 60  
QY 61 AOKFQGRVTMTTRDTSISTAYMELSSLRSRSDTAIYYCVRGFGYSYNYDYYYGMDVWGQGT 119  
Db 61 AOKFQGRVTMTTRNTSISTAYMELSSLRSRSDTAIYYCAREGIAVAGTYYTYYGMDVWGQGT 120  
QY 120 TVTVSS 125  
Db 121 TVTVSS 126  
RESULT 15  
AEK98538  
ID AEK98538 standard; protein; 123 AA.  
XX AC AEK98538;  
XX DT 30-NOV-2006 (first entry)  
XX DE Human anti-Ten-M2 antibody heavy chain variable region, SEQ ID:50.  
XX KW monoclonal antibody; antibody therapy; Ten-M2; diagnosis; pharmaceutical;  
KW tumor; cytostatic; neoplasm; cancer; heavy chain variable region.  
XX OS Homo sapiens.  
XX PN WO2006104978-A2.  
XX PD 05-OCT-2006.  
XX PF 27-MAR-2006; 2006WO-US011031.  
XX PR 25-MAR-2005; 2005US-0665592P.  
XX PA (CURA-) CURAGEN CORP.  
PA (ABGE-) ABGENIX INC.  
XX FI Ettenberg S, Masterman S, Larochele W, Zhong H;  
DR WPI; 2006-670467/69.  
XX DR  
XX PT New fully human monoclonal antibody that binds to Ten-M2 and neutralizes  
PT Ten-M2 activity, useful for treating symptoms and conditions associated  
PT with Ten-M2 activity, e.g. cancer.  
XX  
PS Claim 5; SEQ ID NO 50; 141pp; English.  
XX  
CC The new invention relates to a fully human monoclonal antibody or its  
CC binding fragment that binds to Ten-M2 and neutralizes Ten-M2 activity.  
CC Also described are a method for assaying the level of Ten-M2 in a patient  
CC sample; a composition comprising the antibody or its binding fragment and  
CC a pharmaceutical carrier; and a method of treating malignant tumors. The  
CC antibody is a full-length antibody. Alternatively, the human monoclonal  
CC antibody that binds to Ten-M2 comprises a heavy chain having an amino  
CC acid sequence selected from any of fully defined 116-127 amino acid  
CC sequences (SEQ ID NO. 2, 6, 10, 14, 18, 22, 26, 30, 34, 42, 46, or  
CC 50) given in the specification. It also comprises a light chain having an  
CC amino acid sequence selected from any of fully defined 101-113 amino acid  
CC sequences (SEQ ID NO. 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, or  
CC 52) given in the specification. Alternatively, the antibody or its  
CC binding fragment binds to Ten-M2, where the antibody or binding fragment  
CC neutralizes a Ten-M2-induced activity, and where the antibody or binding  
CC fragment cross-reacts with a fully human anti-Ten-M2 antibody selected  
CC from Mab120, Mab140, and Mab171, Mab179, Mab199, Mab213, or an antibody  
CC in the same antigen-binding bin as fully human anti-Ten-M2 antibody  
CC Mab120, Mab140, and Mab171, Mab179, Mab199, or Mab213. Assaying the level  
CC of Ten-M2 in a patient sample comprises contacting the patient sample  
CC with the anti-Ten-M2 antibody, and determining the presence or amount of  
CC anti-Ten-M2 antibody bound to Ten-M2, thus detecting the level of Ten-M2  
CC in the patient sample. The antibodies can be used for treating symptoms  
CC and conditions associated with Ten-M2 activity, e.g. cancer. This

CC sequence is a human anti-Ten-M2 antibody heavy chain variable region  
CC protein sequence.  
XX  
SQ Sequence 123 AA;  
Query Match 87.5%; Score 588; DB 10; Length 123;  
Best Local Similarity 89.6%; Pred. No. 1.9e-46;  
Matches 112; Conservative 5; Mismatches 6; Indels 2; Gaps 1;  
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVQRATQGGLEWGMWNPNSGNTDY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVQRATQGGLEWGMWNPNSGNTGY 60  
QY 61 AOKFQGRVTMTTRDTSISTAYMELSSLRSRSDTAIYYCVRGFGYSYNYDYYYGMDVWGQGT 120  
Db 61 AOKFQGRVTMTTRNTSISTAYMELSSLRSRSDTAIYYCARGPGGSFY--YYGMDVWGQGT 118  
QY 121 TVTVSS 125  
Db 119 TVTVSS 123

Search completed: April 25, 2007, 04:05:20  
Job time : 109.404 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 10 Seconds  
(without alignments)  
1261.509 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....YDYVGMVWGQGTITVTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	82.9	127	2 S34014	Ig heavy chain V r
2	537.5	80.0	136	2 S31600	Ig heavy chain V r
3	534	79.5	129	2 S46393	Ig heavy chain V r
4	516.5	76.9	118	2 S36265	Ig heavy chain V-1
5	515	76.6	123	2 D33548	Ig heavy chain V r
6	514	76.5	129	2 S36260	Ig heavy chain V r
7	511.5	76.1	135	2 S49530	anti-Sm antibody V
8	510.5	76.0	132	2 S31596	Ig heavy chain V r
9	500	74.4	131	2 S26792	Ig heavy chain V r
10	499	74.3	119	2 PH0961	Ig heavy chain V r
11	496.5	73.9	110	2 PH1670	Ig heavy chain V r
12	496	73.8	98	2 S26918	Ig heavy chain V r
13	495.5	73.7	132	2 PH0954	Ig heavy chain V r
14	495.5	73.7	171	2 S23623	Ig heavy chain V r
15	494.5	73.6	118	2 PH1666	Ig heavy chain V r
16	493.5	73.4	136	2 PH0960	Ig heavy chain V r
17	488.5	72.7	143	1 E1HUND	Ig heavy chain pre
18	488	72.6	127	2 PH0955	Ig heavy chain V r
19	487.5	72.5	124	2 S19665	Ig heavy chain V r
20	486	72.3	133	2 C33548	Ig heavy chain V-1
21	486	72.3	627	2 S14683	Ig mu chain precu
22	484	72.0	142	2 A32483	Ig heavy chain V r
23	480	71.4	122	2 S36271	Ig heavy chain V r
24	480	71.4	160	2 PL0105	anti-PR2 erythrocy
25	477.5	71.1	126	2 B33548	Ig heavy chain V-1
26	476.5	70.9	114	2 PH1667	Ig heavy chain V r
27	473.5	70.5	128	2 PH0952	Ig heavy chain V r
28	472.5	70.3	120	2 S31999	Ig heavy chain V r
29	468	69.6	109	2 PH1668	Ig heavy chain V r

#### ALIGNMENTS

##### RESULT 1

S34014

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996

C;Accession: S34014; S30535

R;Marette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A;Reference number: S34001; MUID:93209281; PMID:7681398

A;Accession: S34014

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-127 <VAR>

A;Cross-references: UNIPARC:UPI0000176D31; EMBL:Z18321

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 557; DB 2; Length 127;

Best Local Similarity 82.7%; Pred. No. 1.4e-42;

Matches 105; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

```

Qy 1 QVQLVQSGAEVKKPGASVKASGVTFTSYDINWVRQATGQGLEWGMWNPNSGNTDY 60
Db 1 QVQMVQSGAEVKKPGASVKASGVTFTSYDINWVRQATGQGLEWGMWNPSSGNTGY 60
Qy 61 AQKFGKRVMTTRDTSISTAYMELSSLRSEDTAIYCVR--GFGYSYNYDYVYGMVWGQ 118
Db 61 AQKFGKRVMTTRDTSISTAYMELSSLRSEDTAVYFCARALSIGVAVIRGYTALDVWGQ 120
Qy 119 TTVTVSS 125
Db 121 TTVSVSS 127

```

##### RESULT 2

S31600

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S31600

R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the

A;Reference number: S31585

A;Accession: S31600

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-136 <CUI>

A;Cross-references: UNIPARC:UPI0000116453; EMBL:Z14165; NID:q30994; PIDN:CAA78534.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 537.5; DB 2; Length 136;  
Best Local Similarity 82.4%; Pred. No. 8.1e-41;  
Matches 103; Conservative 6; Mismatches 7; Indels 9; Gaps 1;  
  
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGLEWMGWINPNSGNTDY 60  
DB 20 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGLEWMGWINPNSGNTGY 79  
  
QY 61 AQKFGQGVVTRDTSISTAYMELSLRSRSDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120  
DB 80 AQKFGQGVVTRDTSISTAYMELSLRSRSDTAIYYCAR-----WRDAFDWGQGT 130  
  
QY 121 VTVSS 125  
DB 131 VTVSS 135

## RESULT 3

S46393  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S46393  
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A:Reference number: S46390; MUID:94254092; PMID:8196048  
A:Accession: S46393  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-129 <FIG>  
A:Cross-references: UNIPARC:UPI000011663A; EMBL:Z31680; NID:G509786; PIDN:CAA83485.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 534; DB 2; Length 129;  
Best Local Similarity 79.8%; Pred. No. 1.6e-40;  
Matches 103; Conservative 7; Mismatches 15; Indels 4; Gaps 1;  
  
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGLEWMGWINPNSGNTDY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWINPNSGNTNY 60  
  
QY 61 AQKFGQGVVTRDTSISTAYMELSLRSRSDTAIYYCVRGFGYSYNDYYG---MDVWG 116  
DB 61 AQKFGQGVVTRDTSISTAYMELSLRSRSDTAIYYCARSSAYYDSSGGYSANYMDVWG 120  
  
QY 117 QGTVTVSS 125  
DB 121 KGTTVTVSS 129

## RESULT 4

S36265  
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C:Accession: S36265  
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MUID:93178448; PMID:7679990  
A:Accession: S36265  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-118 <GRI>  
A:Cross-references: UNIPARC:UPI0000118DE8; EMBL:Z18846; NID:G33121; PIDN:CAA79298.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 516.5; DB 2; Length 118;  
Best Local Similarity 80.0%; Pred. No. 5.1e-39;  
Matches 100; Conservative 6; Mismatches 12; Indels 7; Gaps 1;  
  
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGLEWMGWINPNSGNTDY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWINPNSGNTNY 60  
  
QY 61 AQKFGQGVVTRDTSISTAYMELSLRSRSDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120  
DB 61 AQKFGQGVVTRDTSISTAYMELSLRSRSDTAIYYCARDFLSGY-----LDYWGQGT 113  
  
QY 121 VTVSS 125  
DB 114 VTVSS 118

## RESULT 5

D33548  
Ig heavy chain V-1 region (WIL2) - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
C:Accession: D33548  
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expres  
A:Reference number: A33548; MUID:89345575; PMID:2503826  
A:Accession: D33548  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-123 <KIP>  
A:Cross-references: UNIPARC:UPI0000176909  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 515; DB 2; Length 123;  
Best Local Similarity 78.6%; Pred. No. 7.2e-39;  
Matches 99; Conservative 10; Mismatches 13; Indels 4; Gaps 2;  
  
QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGLEWMGWINPNSGNTDY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVVRQAPGQGLEWMGWINPNSGNTNY 60  
  
QY 61 AQKFGQGVVTRDTSISTAYMELSLRSRSDTAIYYCVRGFGYSY-NYDYYGMDVWGQGT 119  
DB 61 AEKFGQGVVTRDTSINTAYMELSLRLSDTAIYYCARA---SYCGYDCYFFDYWGQGT 117  
  
QY 120 TVTVSS 125  
DB 118 LVTVSS 123

## RESULT 6

S36260  
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C:Accession: S36260  
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MUID:93178448; PMID:7679990  
A:Accession: S36260  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-129 <GRI>  
A:Cross-references: UNIPARC:UPI0000118DEB; EMBL:Z18851; NID:G33124; PIDN:CAA79303.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 514; DB 2; Length 129;  
Best Local Similarity 78.3%; Pred. No. 9.3e-39;  
Matches 101; Conservative 8; Mismatches 16; Indels 4; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60  
|||  
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60  
|||  
QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRLSDTAIYYCVRG-FGFSYNYD---YYGMDVWG 116  
|||  
DB 61 AQKFGQGRVTMTSDTSISTAYMELSLRLSDTAIYYCVRG-FGFSYNYD---YYGMDVWG 120  
|||  
QY 117 QGTTVTSS 125  
|||  
DB 121 KGTITVSS 129  
|||

RESULT 7  
S49530  
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 23-Jul-1999  
C:Accession: S49530  
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
submitted to the EMBL Data Library, October 1994  
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.  
A:Reference number: S48797  
A:Accession: S49530  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-135 <MA>  
A:Cross-references: UNIPARC:UPI00001166FF; EMBL:Z46348; NID:G560839; PIDN:CAA86467.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 511.5; DB 2; Length 135;  
Best Local Similarity 79.4%; Pred. No. 1.6e-38;  
Matches 100; Conservative 6; Mismatches 9; Indels 11; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60  
|||  
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 79  
|||  
QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRLSDTAIYYCVRG-FGFSYNYDYYGMDVWGQGT 119  
|||  
DB 80 AQKFGQGRVTMTSDTSISTAYMELSLRLSDTAIYYCVRG-FGFSYNYDYYGMDVWGQGT 129  
|||  
QY 120 TTVTSS 125  
|||  
DB 130 LTVSS 135  
|||

RESULT 8  
S31596  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31596  
R:Cuinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnel, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31596  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-132 <CU>  
A:Cross-references: UNIPARC:UPI0000116454; EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 510.5; DB 2; Length 132;

Best Local Similarity 79.2%; Pred. No. 1.9e-38;  
Matches 99; Conservative 6; Mismatches 7; Indels 13; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60  
|||  
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 79  
|||  
QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRLSDTAIYYCVRG-FGFSYNYDYYGMDVWGQGT 120  
|||  
DB 80 AQKFGQGRVTMTSDTSISTAYMELSLRLSDTAIYYCVRG-FGFSYNYDYYGMDVWGQGT 126  
|||  
QY 121 TTVSS 125  
|||  
DB 127 TTVSS 131  
|||

RESULT 9  
S26792  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26792  
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
Eur. J. Immunol. 22, 241-245, 1992  
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami  
A:Reference number: S26786; MUID:92111632; PMID:1730251  
A:Accession: S26792  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-131 <MOR>  
A:Cross-references: UNIPARC:UPI0000115FC3; EMBL:X61012; NID:G32804; PIDN:CAA43346.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 500; DB 2; Length 131;  
Best Local Similarity 72.5%; Pred. No. 1.6e-37;  
Matches 95; Conservative 13; Mismatches 17; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60  
|||  
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60  
|||  
QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRLSDTAIYYCVRG-FGFSYNYDYYGMDV 114  
|||  
DB 61 AQKFGQGRVTMTSDTSISTAYMELSLRLSDTAIYYCVRG-FGFSYNYDYYGMDV 120  
|||  
QY 115 WGGTITVSS 125  
|||  
DB 121 WGGTITVSS 131  
|||

RESULT 10  
PH0961  
Ig heavy chain V region (G6+ T-L33) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C:Accession: PH0961  
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291  
A:Accession: PH0961  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-119 <MA>  
A:Cross-references: UNIPARC:UPI0000176CE5  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: framework 2







Query Match 73.7%; Score 495.5; DB 2; Length 171;  
 Best Local Similarity 70.9%; Pred. No. 5.5e-37;  
 Matches 95; Conservative 9; Mismatches 13; Indels 17; Gaps 2;

QY 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 20 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 79  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AQKFGSRVTMTSDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYG----- 111  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 80 GQKFGSRVTMTSDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYG----- 111  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 112 MDVWGQGTITVTVSS 125  
 :||||| |||||  
 Db 132 FDIWGQGTITVTVSS 145  
 :||||| |||||

RESULT 15  
 PHI666  
 Ig heavy chain V region (clone 6C9) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
 C:Accession: PHI666  
 R: Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
 J. Exp. Med. 178, 331-336, 1993  
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
 A:Reference number: PHI642; MUID:93301610; PMID:8315388  
 A:Accession: PHI666  
 A:Molecule type: mRNA  
 A:Residues: 1-118 <HIL>  
 A:Cross-references: UNIPARC:UPI0000176BE7  
 A:Experimental source: B cell  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F; 7-90/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 494.5; DB 2; Length 118;  
 Best Local Similarity 80.5%; Pred. No. 4.5e-37;  
 Matches 95; Conservative 6; Mismatches 16; Indels 1; Gaps 1;

QY 9 AEVKKPGASVKVSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAQKFGSRV 68  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 AEVKKPGASVKVSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAQKFGSRV 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 69 TMTSDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGTITVTVSS 125  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 61 TITRDTASTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGTITVTVSS 118  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: April 25, 2007, 04:06:39  
 Job time : 9.5339 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 85 Seconds  
(without alignments)  
1574.822 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....YDYFGMDVWGQGTITVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 8.4.\*

1: uniprot\_eprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	497.5	74.0	159	2	Q9GQSO HUMAN	Q9GQSO homo sapien
2	494	73.5	119	2	Q9UL94 HUMAN	Q9UL94 homo sapien
3	494	73.5	125	2	Q9UL95 HUMAN	Q9UL95 homo sapien
4	491	73.1	244	2	Q6SZC8 HUMAN	Q6SZC8 homo sapien
5	488.5	72.7	147	1	HVIC HUMAN	P01744 homo sapien
6	481.5	71.7	124	2	Q9UL92 HUMAN	Q9UL92 homo sapien
7	478.5	71.2	498	2	Q6N041 HUMAN	Q6N041 homo sapien
8	474	70.5	497	2	Q8FY24 HUMAN	Q8FY24 homo sapien
9	470.5	70.0	500	2	Q9BRV0 HUMAN	Q9BRV0 homo sapien
10	457.5	68.1	518	2	Q6N030 HUMAN	Q6N030 homo sapien
11	455	67.7	119	2	Q9GYZ2 MOUSE	Q9GYZ2 mus musculus
12	446	66.4	500	2	Q6N091 HUMAN	Q6N091 homo sapien
13	441	65.6	117	1	HVIG HUMAN	P23083 homo sapien
14	440	65.5	117	1	HVIB HUMAN	P01743 homo sapien
15	438	65.2	480	2	Q6F089 HUMAN	Q6F089 homo sapien
16	436	64.9	458	2	Q5BJZ2 RAT	Q5BJZ2 rattus norv
17	433.5	64.5	469	2	Q7Z7P5 MOUSE	Q7Z7P5 mus musculus
18	430	64.0	481	2	Q9LW18 MOUSE	Q9LW18 mus musculus
19	429.5	63.9	116	2	Q9UL89 HUMAN	Q9UL89 homo sapien
20	425.5	63.3	145	2	Q924R4 MOUSE	Q924R4 mus musculus
21	425	63.2	519	2	Q5BEM2 HUMAN	Q5BEM2 homo sapien
22	424.5	63.2	617	2	Q4KML5 MOUSE	Q4KML5 mus musculus
23	422	62.8	147	2	Q925S3 MOUSE	Q925S3 mus musculus
24	420	62.5	157	2	Q95978 HUMAN	Q95978 homo sapien
25	419.5	62.4	475	2	Q6N095 HUMAN	Q6N095 homo sapien
26	419	62.4	470	2	Q7FMK1 MOUSE	Q7FMK1 mus musculus
27	418.5	62.3	118	1	HVSI MOUSE	P06330 mus musculus
28	418	62.2	117	2	Q9QXE9 MOUSE	Q9QXE9 mus musculus
29	417	62.1	472	2	Q6PJ47 MOUSE	Q6PJ47 mus musculus
30	417	62.1	473	2	Q9DBL4 MOUSE	Q9DBL4 mus musculus
31	416.5	62.0	463	2	Q99LCA4 MOUSE	Q99LCA4 mus musculus

32	415.5	61.8	145	2	Q924Q6 MOUSE	Q924Q6 mus musculus
33	414	61.6	117	1	HV12 MOUSE	P01756 mus musculus
34	414	61.6	146	2	Q924Q3 MOUSE	Q924Q3 mus musculus
35	413.5	61.5	145	2	Q924R1 MOUSE	Q924R1 mus musculus
36	413	61.5	120	1	HV03 MOUSE	P01747 mus musculus
37	413	61.5	468	2	Q569F9 MOUSE	Q569F9 mus musculus
38	412.5	61.4	143	2	Q924Q5 MOUSE	Q924Q5 mus musculus
39	412.5	61.4	145	2	Q924R3 MOUSE	Q924R3 mus musculus
40	412.5	61.4	613	2	Q8VCX7 MOUSE	Q8VCX7 mus musculus
41	412	61.3	134	2	Q65ZK6 MOUSE	Q65ZK6 mus musculus
42	410.5	61.1	145	2	Q924Q9 MOUSE	Q924Q9 mus musculus
43	410	61.0	598	2	Q568Y0 RAT	Q568Y0 rattus norv
44	409.5	60.9	143	2	Q924R0 MOUSE	Q924R0 mus musculus
45	409.5	60.9	465	2	Q6PJB2 MOUSE	Q6PJB2 mus musculus

## ALIGNMENTS

### RESULT 1

Q9GQSO HUMAN  
ID Q9GQSO\_HUMAN PRELIMINARY; PRT; 159 AA.  
AC Q9GQSO;  
DT 01-DEC-2001, integrated into UniProtKB/TREMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 18-APR-2006, entry version 21.  
DE Putative matrix cell adhesion molecule-3.  
DE OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Tilson M.D.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AY039025; AAK82649.1; -; mRNA.  
DR HSSP; P01869; 1AE6.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig sub.  
DR InterPro; IPR013106; Ig\_V-set.  
DR InterPro; IPR003596; Ig\_V-set\_sub.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain.  
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;  
Query Match 74.0%; Score 497.5; DB 2; Length 159;  
Best Local Similarity 74.0%; Pred. No. 1e-41;  
Matches 97; Conservative 12; Mismatches 15; Indels 7; Gaps 2;

QY	1	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGNPNNGNTDY	60
DB	20	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGNPNNGNTDY	79
QY	61	AKFGQRTVTRDTSTSTAYMELSSRLSEDTAIYVCVR-----GFQSYNYDYGYMDV	114
DB	80	SKQFQRLTWRDTSTSTAYMELSSRLSEDTAIYVCVR-----GFQSYNYDYGYMDV	138
QY	115	WGQGTITVTVSS 125	
DB	139	WGQGTITVTVSS 149	

### RESULT 2

Q9UL94 HUMAN  
ID Q9UL94\_HUMAN PRELIMINARY; PRT; 119 AA.

```

AC Q9UL94;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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DR EMBL; AF035020; AAD56256.1; -; mRNA.
DR HSSP; P01751; INOB.
DR SMR; Q9UL94; 1-116.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119
FT NON_TER 1
SQ SEQUENCE 119 AA; 13205 MW; 13B64F5345F4A16E CRC64;

Query Match 73.5%; Score 494; DB 2; Length 119;
Best Local Similarity 76.0%; Pred. No. 1.7e-41;
Matches 95; Conservative 10; Mismatches 14; Indels 6; Gaps 1;

QY 1 QVQLVSGAEVKPGASVKASCTFTSYDINWVROATCGLEWGMWNPNSGNTDY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 EVQLVESGAEVKPGASVKASCTFTGYTHWVRQAPGQGLEWGMWNPNSWTNY 60
QY 61 AQKFGQVMTWTRDTSISTAYMELSLRSDDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 AQKFGQVMTWTRDTSISTAYMELSLRSDDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
QY 121 VTVSS 125
Db :||||
115 VTVSS 119

RESULT 3
Q9UL95 HUMAN PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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DR EMBL; AF035020; AAD56256.1; -; mRNA.
DR HSSP; P01751; INOB.
DR SMR; Q9UL94; 1-116.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119
FT NON_TER 1
SQ SEQUENCE 119 AA; 13205 MW; 13B64F5345F4A16E CRC64;

Query Match 73.5%; Score 494; DB 2; Length 119;
Best Local Similarity 76.0%; Pred. No. 1.7e-41;
Matches 95; Conservative 10; Mismatches 14; Indels 6; Gaps 1;

QY 1 QVQLVSGAEVKPGASVKASCTFTSYDINWVROATCGLEWGMWNPNSGNTDY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 EVQLVESGAEVKPGASVKASCTFTGYTHWVRQAPGQGLEWGMWNPNSWTNY 60
QY 61 AQKFGQVMTWTRDTSISTAYMELSLRSDDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 AQKFGQVMTWTRDTSISTAYMELSLRSDDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
QY 121 VTVSS 125
Db :||||
115 VTVSS 119

RESULT 4
Q65ZC8 HUMAN PRELIMINARY; PRT; 244 AA.
AC Q65ZC8;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 18-APR-2006, entry version 10.
DE Single-chain Fv (Fragment).
DE Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
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DR EMBL; Y13057; CAA73500.1; -; mRNA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR Pfam; PF07686; V-set; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.

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RT RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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-----
DR EMBL; AF035019; AAD56255.1; -; mRNA.
DR HSSP; P01751; INOB.
DR SMR; Q9UL95; 1-122.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 125
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 73.5%; Score 494; DB 2; Length 125;
Best Local Similarity 76.0%; Pred. No. 1.8e-41;
Matches 95; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKPGASVKASCTFTSYDINWVROATCGLEWGMWNPNSGNTDY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 EVQLVESGAEVKPGASVKASCTFTGYTHWVRQAPGQGLEWGMWNPNSGNTNY 60
QY 61 AQKFGQVMTWTRDTSISTAYMELSLRSDDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 AQKFGQVMTWTRDTSISTAYMELSLRSDDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
QY 121 VTVSS 125
Db :||||
121 VTVSS 125

RESULT 4
Q65ZC8 HUMAN PRELIMINARY; PRT; 244 AA.
AC Q65ZC8;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 18-APR-2006, entry version 10.
DE Single-chain Fv (Fragment).
DE Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
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DR EMBL; Y13057; CAA73500.1; -; mRNA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR Pfam; PF07686; V-set; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.

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KW Immunoglobulin domain.  
FT NON\_TER 1 1  
FT NON\_TER 244 244  
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;  
Query Match 73.1%; Score 491; DB 2; Length 244;  
Best Local Similarity 75.4%; Pred. No. 7.5e-41; Mismatches 12; Indels 6; Gaps 2;  
Matches 95; Conservative 13; Mismatches 12; Indels 6; Gaps 2;  
QY 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTDY 60  
DB 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTDY 60  
QY 61 AQKFGQVRVMTTRDTSISTAYMELSSLRSEDTAIYICVR-GFGYSYNDYYGMDVWGQGT 119  
DB 61 AQKFGQVRVMTTRDTSISAAAYMEVSLRSDDTAVYICAREGTGSA-----IYGMVDVWGQGT 115  
QY 120 TVTVSS 125  
DB 116 LVTVSS 121  
RESULT 5  
HVIC\_HUMAN STANDARD; PRT; 147 AA.  
ID HVIC\_HUMAN PRELIMINARY; PRT; 124 AA.  
AC P01744;  
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
DT 01-DEC-2000, sequence version 2.  
DT 30-MAY-2006, entry version 47.  
DE Ig heavy chain V-I region ND precursor (Fragments).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83065234; PubMed=6815656;  
RA Kenten J.H., Molsgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
RA Bell L.O., Gould H.J.;  
RT "Cloning and sequence determination of the gene for the human  
RT immunoglobulin epsilon chain expressed in a myeloma cell line."  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).  
RN [2]  
RP PROTEIN SEQUENCE OF 20-147.  
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RL (in) Bach M.K. (eds.);  
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
RL Marcel Dekker, New York (1978).  
CC -!- MISCELLANEOUS: This epsilon chain was isolated from a myeloma  
CC protein.  
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
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HSSP; P01751; INQB.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig\_sub.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region; Pyroglutamate carboxylic acid; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 147  
FT DOMAIN 20 131  
FT MOD\_RES 20 20  
FT Ig heavy chain V-I region ND.  
FT /FTID=PRO\_0000015246.  
FT Ig-like  
FT Pyroglutamate carboxylic acid.

FT DISULFID 41 115  
FT CONFLICT 21 21  
FT CONFLICT 53 54  
FT CONFLICT 67 68  
FT CONFLICT 125 125  
FT NON\_TER 147 147  
SQ SEQUENCE 147 AA; 16496 MW; 948F9F72A5366C20 CRC64;  
Query Match 72.7%; Score 488.5; DB 1; Length 147;  
Best Local Similarity 70.3%; Pred. No. 7.6e-41;  
Matches 90; Conservative 16; Mismatches 19; Indels 3; Gaps 1;  
QY 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTDY 60  
DB 20 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTDY 79  
QY 61 AQKFGQVRVMTTRDTSISTAYMELSSLRSEDTAIYICVRG---FGYSYNDYYGMDVWGQ 117  
DB 80 AQKFGQVRVMTTRDTSISTAYMELSSLRSEDTAIYICVRG---FGYSYNDYYGMDVWGQ 139  
QY 118 GTTVTVSS 125  
DB 140 GTTVTVSS 147  
RESULT 6  
Q9UL92\_HUMAN  
ID Q9UL92\_HUMAN PRELIMINARY; PRT; 124 AA.  
AC Q9UL92;  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DT 18-APR-2006, entry version 22.  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
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EMBL; AF035022; AAD56258.1; -; mRNA.  
DR HSSP; P01751; INQB.  
DR LinkHub; Q9UL92;  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig\_sub.  
DR InterPro; IPR013106; Ig\_V-set.  
DR InterPro; IPR003596; Ig\_V-set\_sub.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin domain.  
FT NON\_TER 1 1  
FT NON\_TER 124 124  
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;  
Query Match 71.7%; Score 481.5; DB 2; Length 124;  
Best Local Similarity 76.0%; Pred. No. 3.1e-40;  
Matches 95; Conservative 9; Mismatches 20; Indels 1; Gaps 1;  
QY 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTDY 60  
DB 1 EVQLVESGAEVKPKGASVKVSKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTDY 60

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QY 61 AQKFGQGRVTMTDRTSISTAYMELSLRSEDIAIYVCVRGFGSYNDYVYGGMDVWGQGT 120
DB 61 AQKFGQGRVTMTDRTSISTAYMELSLRSEDIAIYVCVRGFGSYNDYVYGGMDVWGQGT 119
QY 121 VTVSS 125
DB 120 VTVSS 124

RESULT 7
Q6N041 HUMAN PRELIMINARY; PRT; 498 AA.
AC Q6N041;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 18-APR-2006, entry version 13.
DE Hypothetical protein DKFZp686016217 (Fragment).
GN Name=DKFZp686016217;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weill B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BX6407110; CAE45829.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q6N041; 268-476.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR KW Hypothetical protein; Immunoglobulin domain; Repeat.
FT NON TR 1
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;

Query Match 71.2%; Score 478.5; DB 2; Length 498;
Best Local Similarity 74.6%; Pred. NO. 3.1e-39;
Matches 94; Conservative 11; Mismatches 18; Indels 3; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 35 QVQLVQSGADVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGPPEWMGMINPRDGSYKY 94

QY 61 AQKFGQGRVTMTDRTSISTAYMELSLRSEDIAIYVCVR- - - - -GFGYSYNDYVYGGMDVWGQGT 119
DB 95 AQKFGQGRVTMTDRTSISTAYMELSLRSEDIAIYVCVR- - - - -GFGYSYNDYVYGGMDVWGQGT 119

QY 120 VTVSS 125
DB 153 LVTSS 158

RESULT 8
Q6N041 HUMAN PRELIMINARY; PRT; 498 AA.
AC Q6N041;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 18-APR-2006, entry version 13.
DE Hypothetical protein DKFZp686016217 (Fragment).
GN Name=DKFZp686016217;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weill B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BX6407110; CAE45829.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q6N041; 268-476.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR KW Hypothetical protein; Immunoglobulin domain; Repeat.
FT NON TR 1
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;

Query Match 71.2%; Score 478.5; DB 2; Length 498;
Best Local Similarity 74.6%; Pred. NO. 3.1e-39;
Matches 94; Conservative 11; Mismatches 18; Indels 3; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 35 QVQLVQSGADVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGPPEWMGMINPRDGSYKY 94

QY 61 AQKFGQGRVTMTDRTSISTAYMELSLRSEDIAIYVCVR- - - - -GFGYSYNDYVYGGMDVWGQGT 119
DB 95 AQKFGQGRVTMTDRTSISTAYMELSLRSEDIAIYVCVR- - - - -GFGYSYNDYVYGGMDVWGQGT 119

QY 120 VTVSS 125
DB 153 LVTSS 158

RESULT 9
Q6N041 HUMAN PRELIMINARY; PRT; 500 AA.
AC Q6N041;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 25-JUL-2006, entry version 36.
DE IGHA1 protein.
GN Name=IGHA1;
OS Homo sapiens (Human).

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Q6WY24 HUMAN PRELIMINARY; PRT; 497 AA.
AC Q6WY24;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 27-JUN-2006, entry version 25.
DE SMC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -----
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CC -----
DR EMBL; AF283666; AAL36987.1; -; mRNA.
DR HSSP; P01876; 1OW0.
DR SMR; Q6WY24; 267-475.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR KW Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SQ SEQUENCE 497 AA; 53666 MW; F24D08DFAS663E5 CRC64;

Query Match 70.5%; Score 474; DB 2; Length 497;
Best Local Similarity 70.0%; Pred. NO. 8.6e-39;
Matches 91; Conservative 13; Mismatches 16; Indels 10; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 20 QEQLQSGAEVTKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGMNPTGNTGF 79

QY 61 AQKFGQGRVTMTDRTSISTAYMELSLRSEDIAIYVCVR- - - - -GFGYSYNDYVYGGMDVW 115
DB 80 AQKFGQGRVTMTDRTSISTAYMELSLRSEDIAIYFCARGNLRCGRGFGYNW- - - - -FDPW 134

QY 116 GQGTTVTVSS 125
DB 135 GHGTLTVSS 144

RESULT 9
Q6WY24 HUMAN PRELIMINARY; PRT; 500 AA.
AC Q6WY24;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 25-JUL-2006, entry version 36.
DE IGHA1 protein.
GN Name=IGHA1;
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Prostate;  
RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
RG Mammalian Gene Collection Program Team;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Schenck C.M., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Prostate;  
RG NIH MGC Project;  
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL; BC005951; AAH05951.1; -; mRNA.  
DR HSP; P01876; IOW0.  
DR SMR; Q9BRV0; 25-300, 270-478.  
DR Ensembl; ENSG00000130076; Homo sapiens.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0030106; P:MHC class I receptor activity; IEA.  
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.  
DR InterPro; IPR013151; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_C1-set.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR013106; Ig\_V-set.  
DR InterPro; IPR003596; Ig\_V-set\_sub.  
DR Pfam; PF07654; C1-set; 2.  
DR Pfam; PF00047; Ig; 1.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG1; 1.  
DR SMART; SM00407; IG1; 2.  
DR SMART; SM00406; IG1; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;  
Query Match 70.0%; Score 470.5; DB 2; Length 500;  
Best Local Similarity 71.9%; Pred. No. 2e-38;  
Matches 92; Conservative 11; Mismatches 22; Indels 3; Gaps 2;  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWVGWGINPNSGNTDY 60  
DB 20 QVHLVQSGAEVMPGASVRVSKTSYGFHTYSIIWVRQAPGQLEWVGWISPSDNTFR 79  
QY 61 AQKFGQGRVTMTDTSISTAYMELSSLRSEDATLYYCVRGF-GYS---YNYDYGGMDVWGQ 117

Db 80 AKKFGQGRVTMTDTSISTAYMELSSLRSDDTANTYICARRYCSYSCQNDYTYYYMDVWGK 139  
QY 118 GTTIVTSS 125  
Db 140 GTTIVTSS 147

RESULT 10  
Q6N030 HUMAN  
ID Q6N030\_HUMAN PRELIMINARY; PRT; 518 AA.  
AC Q6N030;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 27-JUN-2006, entry version 19.  
DE Hypothetical protein DKFp686l15212.  
GN Name=DKFp686l15212;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Rectum tumor;  
RG The German cDNA Consortium;  
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
CC histocompatibility complex class I molecules (By similarity).  
CC -----  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; BX640724; CAB45841.1; -; mRNA.  
DR HSP; P01861; IADQ.  
DR LinkHub; Q6N030;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0030106; P:MHC class I receptor activity; IEA.  
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.  
DR InterPro; IPR000005; HTHArAc.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_C1-set.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003599; Ig\_sub.  
DR InterPro; IPR013106; Ig\_V-set.  
DR InterPro; IPR003596; Ig\_V-set\_sub.  
DR Pfam; PF07654; C1-set; 3.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG1; 1.  
DR SMART; SM00407; IG1; 2.  
DR SMART; SM00406; IG1; 1.  
DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; UNKNOWN 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;  
KW Transmembrane.  
SQ SEQUENCE 518 AA; 57020 MW; 93BF98613BF6382 CRC64;  
Query Match 68.1%; Score 457.5; DB 2; Length 518;  
Best Local Similarity 71.2%; Pred. No. 4.1e-37;  
Matches 89; Conservative 10; Mismatches 23; Indels 3; Gaps 1;  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWVGWGINPNSGNTDY 60  
DB 20 QVHLVQSGAEVKKPGASVKVSCTAGYPTTFHFINWVRQAPGQSGLEWVGINTGNTKY 79  
QY 61 AQKFGQGRVTMTDTSISTAYMELSSLRSEDATLYYCVRGF-GYS---YNYDYGGMDVWGQ 120  
DB 80 SQKFGQGRVTITRTTITATMDLSSLRSEDATVTCARDAPQGVTTTF---DIWQGTGL 136

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QY 121 VTSS 125
DB 137 VTSS 141

RESULT 11
Q9GY22 MOUSE PRELIMINARY; PRT; 119 AA.
AC Q9GY22, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
DE chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBSJ databases.
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CC
EMBL: AF282622; AAG01452.1; -; mRNA.
DR HSP; P01751; IAGW.
DR SMR; Q9GY22; 1-119.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin domain.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA993873FD5FA6AB CRC64;

Query Match 67.7%; Score 455; DB 2; Length 119;
Best Local Similarity 69.6%; Pred. No. 1.4e-37;
Matches 87; Conservative 14; Mismatches 18; Indels 6; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATQGLLEWGMGWINPNSGNTDY 60
DB 1 QVQLVESGAEVKKPGASVKVSCKASGYTFTGYMNVQRQAPGHLEWIGYINPSRGYTN 60
QY 61 AQLKQGRVTMTDTSTISAYMELSLRSEDTHAIYCVRGFGYSYNDYYGMDVVGQGT 120
DB 61 NQKFDKRVTTMTDTSTFSTAYMELSLRSDTSADSAVYTCAR-----YYDDHYCLDYGQGT 114

QY 121 VTSS 125
DB 115 VTSS 119

RESULT 12
Q6N091 HUMAN PRELIMINARY; PRT; 500 AA.
AC Q6N091;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 18-APR-2006, entry version 13.
DE Hypothetical protein DKFP686C02220 (Fragment).
GN Name=DKFP686C02220;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATQGLLEWGMGWINPNSGNTDY 60
DB 1 QVQLVESGAEVKKPGASVKVSCKASGYTFTGYMNVQRQAPGHLEWIGYINPSRGYTN 60
QY 61 AQLKQGRVTMTDTSTISAYMELSLRSEDTHAIYCVRGFGYSYNDYYGMDVVGQGT 120
DB 61 NQKFDKRVTTMTDTSTFSTAYMELSLRSDTSADSAVYTCAR-----YYDDHYCLDYGQGT 114

QY 121 VTSS 125
DB 115 VTSS 119

RESULT 13
HVIG_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1991, sequence version 1.
DT 30-MAY-2006, entry version 38.
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
DE "Dispersed localization of D segments in the human immunoglobulin
DE heavy-chain locus."

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBSJ databases.
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CC
EMBL: BX640625; CAE45779.1; -; mRNA.
DR HSP; P01751; IAGW.
DR SMR; Q6N091; 270-478.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig V-set.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Repeat.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 500 AA; 54160 MW; 3C423A17D65A41E4 CRC64;

Query Match 66.4%; Score 446; DB 2; Length 500;
Best Local Similarity 69.8%; Pred. No. 5.7e-36;
Matches 88; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATQGLLEWGMGWINPNSGNTDY 60
DB 38 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSLRQAPGHLEWIGWISAYSGQTY 97
QY 61 AQLKQGRVTMTDTSTISAYMELSLRSEDTHAIYCVRGFGY-SYNDYYGMDVVGQGT 119
DB 98 AQLKQGRVTMTDTSTISAYMELSLRSDTSADSAVYTCAR-----IWQGT 154

QY 120 VTSS 125
DB 155 VTSS 160

RESULT 13
HVIG_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1991, sequence version 1.
DT 30-MAY-2006, entry version 38.
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
DE "Dispersed localization of D segments in the human immunoglobulin
DE heavy-chain locus."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -----
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CC -----
DR EMBL; BC065733; AAH65733.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; O6P089; 250-458.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1-set.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003599; IG_sub.
DR InterPro; IPR013106; IG_V-set.
DR InterPro; IPR003596; IG_V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
KW Transmembrane.
SQ SEQUENCE 480 AA; 51998 MW; 2E286C57E4F0ED65 CRC64;

Query Match 65.2%; Score 438; DB 2; Length 480;
Best Local Similarity 68.5%; Pred. No. 3.4e-35;
Matches 87; Conservative 13; Mismatches 19; Indels 8; Gaps 2;

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATCGGLEWMGMWINPNSGNTDY 60
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
20 QVQLVQSGAEVKPKGASVKVCKASGYISIDNYIHWRQAPQGLEWMWIRPQNGGTVS 79
QY 61 AQKFGQGRVTMTDRTSISTAYMELSLRSEDTAIYCYVRGFG--YSYNDYDYYGMDVWGQG 118
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
80 AEKFGQGRVTITDTSINTAYMELTSLKSDDTALYCYARGHSDWSSYFDPY-----WGQG 133

QY 119 TTVTVSS 125
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
134 TLTVTVSS 140
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Search completed: April 25, 2007, 04:06:35  
Job time : 85.0989 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:06:51 ; Search time 16 Seconds  
(without alignments)  
696.311 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVLVQSGAEVKKPGASVKV.....YDYYGMDVWGQGTITVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pdp:\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pdp:\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pdp:\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/iaa/H COMB.pdp:\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/iaa/PCTUS COMB.pdp:\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pdp:\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541.5	80.6	120	2	US-09-025-769B-36
2	541.5	80.6	120	2	US-09-025-769B-59
3	541.5	80.6	120	2	US-09-490-070A-36
4	541.5	80.6	120	2	US-09-490-070A-59
5	541.5	80.6	120	2	US-09-490-153-36
6	541.5	80.6	120	2	US-09-490-153-59
7	541.5	80.6	120	2	US-09-490-324-36
8	541.5	80.6	120	2	US-09-490-324-59
9	528	78.6	117	2	US-09-025-769B-22
10	528	78.6	117	2	US-09-490-070A-22
11	528	78.6	117	2	US-09-490-324-22
12	528	78.6	117	2	US-09-490-324-22
13	526	78.3	470	2	US-09-859-053-28
14	513	76.3	125	2	US-09-199-149-3
15	510.5	76.0	128	1	US-08-202-047-22
16	510.5	76.0	128	2	US-08-964-690-22
17	510	75.9	129	1	US-08-561-521-45
18	510	75.9	129	2	US-08-525-539A-77
19	510	75.9	129	5	PCT-US95-01219-45
20	504	75.0	123	2	US-10-330-613A-21
21	502	74.7	123	1	US-08-477-877B-94
22	502	74.7	123	1	US-08-472-281A-94
23	502	74.7	123	1	US-08-477-989B-94
24	502	74.7	123	2	US-09-462-140D-102
25	502	74.7	123	2	US-09-462-140D-105
26	501	74.6	119	1	US-08-561-521-10

27	501	74.6	119	5	PCT-US95-01219-10	Sequence 10, Appl
28	498	74.1	119	2	US-09-438-954-41	Sequence 41, Appl
29	496	73.8	117	2	US-08-545-809A-96	Sequence 96, Appl
30	496	73.8	117	2	US-09-515-697-96	Sequence 96, Appl
31	493.5	73.4	139	1	US-08-253-877C-19	Sequence 19, Appl
32	493.5	73.4	139	1	US-08-452-164A-19	Sequence 19, Appl
33	493.5	73.4	139	2	US-08-603-024-18	Sequence 18, Appl
34	493.5	73.4	139	2	US-08-450-809-14	Sequence 14, Appl
35	487.5	72.5	118	3	US-09-875-221B-13	Sequence 13, Appl
36	487	72.5	96	2	US-10-194-975-3	Sequence 3, Appl
37	487	72.5	121	1	US-08-202-047-23	Sequence 23, Appl
38	487	72.5	121	2	US-08-964-690-23	Sequence 23, Appl
39	482	71.7	119	1	US-08-561-521-12	Sequence 12, Appl
40	482	71.7	119	5	PCT-US95-01219-12	Sequence 12, Appl
41	481	71.6	123	1	US-08-482-882-86	Sequence 86, Appl
42	481	71.6	123	1	US-08-483-389-86	Sequence 86, Appl
43	481	71.6	123	1	US-08-487-113D-86	Sequence 86, Appl
44	481	71.6	123	1	US-08-473-503-86	Sequence 86, Appl
45	481	71.6	123	1	US-08-483-932-86	Sequence 86, Appl

#### ALIGNMENTS

RESULT 1  
US-09-025-769B-36  
; Sequence 36, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-36  
Query Match 80.6%; Score 541.5; DB 2; Length 120;  
Best Local Similarity 84.0%; Pred. No. 1.9e-44;

Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
 Db 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
 Qy 61 AQKFGQGVMTTRDTSISTAYMELSSLSRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120  
 Db 61 AQKFGQGVMTTRDTSISTAYMELSSLSRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120  
 Qy 121 VTVSS 125  
 Db 116 VTVSS 120

RESULT 2

US-09-025-769B-59  
 ; Sequence 59, Application US/09025769B  
 ; Patent No. 6300064  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knappik, Achim  
 ; APPLICANT: Pack, Peter  
 ; APPLICANT: Ilag, Vic  
 ; APPLICANT: Ge, Liming  
 ; APPLICANT: Moroney, Simon  
 ; APPLICANT: Plueckthun, Andreas  
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 ; NUMBER OF SEQUENCES: 373  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10021  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION NUMBER: US/09/025,769B  
 ; FILING DATE: 18-FEB-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 95 11 3021.0  
 ; FILING DATE: 18-AUG-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: James F. Haley, Jr., Esq.  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: MORPHO/5  
 ; TELEPHONE: (212)596-9000  
 ; TELEFAX: (212)596-9090  
 ; INFORMATION FOR SEQ ID NO: 59:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 120 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-025-769B-59

Query Match 80.6%; Score 541.5; DB 2; Length 120;  
 Best Local Similarity 84.0%; Pred. No. 1.9e-44;  
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;  
 Qy 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
 Db 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
 Qy 61 AQKFGQGVMTTRDTSISTAYMELSSLSRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120  
 Db 61 AQKFGQGVMTTRDTSISTAYMELSSLSRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120

Qy 121 VTVSS 125  
 Db 116 VTVSS 120

RESULT 3

US-09-490-070A-36  
 ; Sequence 36, Application US/09490070A  
 ; Patent No. 6696248  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knappik, Achim  
 ; APPLICANT: Pack, Peter  
 ; APPLICANT: Ilag, Vic  
 ; APPLICANT: Ge, Liming  
 ; APPLICANT: Moroney, Simon  
 ; APPLICANT: Plueckthun, Andreas  
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 ; NUMBER OF SEQUENCES: 373  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
 ; STREET: 1666 K Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20006  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/490,070A  
 ; FILING DATE: 24-Jan-2000  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 95 11 3021.0  
 ; FILING DATE: 18-AUG-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Colin G. Sandercock, Esq.  
 ; REGISTRATION NUMBER: 31,298  
 ; REFERENCE/DOCKET NUMBER: 37629-0005  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 912-2000  
 ; TELEFAX: (202) 912-2020  
 ; INFORMATION FOR SEQ ID NO: 36:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 120 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: <Unknown>  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
 ; US-09-490-070A-36

Query Match 80.6%; Score 541.5; DB 2; Length 120;  
 Best Local Similarity 84.0%; Pred. No. 1.9e-44;  
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;  
 Qy 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
 Db 1 QVQLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60  
 Qy 61 AQKFGQGVMTTRDTSISTAYMELSSLSRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120  
 Db 61 AQKFGQGVMTTRDTSISTAYMELSSLSRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120  
 Qy 121 VTVSS 125  
 Db 116 VTVSS 120  
 RESULT 4  
 US-09-490-070A-59

; Sequence 59, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon

; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; White & Mcauliffe  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
; STRANDEDNESS: <Unknown>  
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-490-070A-59

Query Match 80.6%; Score 541.5; DB 2; Length 120;  
Best Local Similarity 84.0%; Pred. No. 1.9e-44;  
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATQGQLEWMGWINPNSGNTDY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATQGQLEWMGWINPNSGNTNY 60  
QY 61 AOKFGRTVMTDTSISTAYMELSLRSEDYIYCVRGFGYSYNDYVYGGMDVWGQTT 120  
Db 61 AOKFGRTVMTDTSISTAYMELSLRSEDYIYCVRGFGYSYNDYVYGGMDVWGQTT 115  
QY 121 VTVSS 125  
Db 116 VTVSS 120

RESULT 5  
US-09-490-153-36  
; Sequence 36, Application US/09490153  
; Patent No. 6706484  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon

; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,153  
; FILING DATE: 24-Jan-2000

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; STRANDEDNESS: <Unknown>

; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-490-153-36

Query Match 80.6%; Score 541.5; DB 2; Length 120;  
Best Local Similarity 84.0%; Pred. No. 1.9e-44;  
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATQGQLEWMGWINPNSGNTDY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATQGQLEWMGWINPNSGNTNY 60  
QY 61 AOKFGRTVMTDTSISTAYMELSLRSEDYIYCVRGFGYSYNDYVYGGMDVWGQTT 120  
Db 61 AOKFGRTVMTDTSISTAYMELSLRSEDYIYCVRGFGYSYNDYVYGGMDVWGQTT 115  
QY 121 VTVSS 125  
Db 116 VTVSS 120

RESULT 6  
US-09-490-153-59  
; Sequence 59, Application US/09490153  
; Patent No. 6706484  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas

/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10021  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/490,153  
/ FILING DATE: 24-Jan-2000  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/025,769B  
/ FILING DATE: 18-FEB-1998  
/ APPLICATION NUMBER: EP 95 11 3021.0  
/ FILING DATE: 18-AUG-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: James F. Haley, Jr., Esq.  
/ REGISTRATION NUMBER: 27,794  
/ REFERENCE/DOCKET NUMBER: MORPHO/5  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212)596-9000  
/ TELEFAX: (212)596-9090  
/ INFORMATION FOR SEQ ID NO: 59:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 120 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-490-153-59  
  
Query Match 80.6%; Score 541.5; DB 2; Length 120;  
Best Local Similarity 84.0%; Pred. No. 1.9e-44;  
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;  
  
QY 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY 60  
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY 60  
  
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120  
Db 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120  
  
QY 121 VTVSS 125  
Db 116 VTVSS 120  
  
RESULT 7  
US-09-490-324-36  
; Sequence 36, Application US/09490324  
; Patent No. 6828422  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,153  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-490-153-59

/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/490,324  
/ FILING DATE: 24-Jan-2000  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/025,769  
/ FILING DATE: 18-FEB-1998  
/ APPLICATION NUMBER: EP 95 11 3021.0  
/ FILING DATE: 18-AUG-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: James F. Haley, Jr., Esq.  
/ REGISTRATION NUMBER: 27,794  
/ REFERENCE/DOCKET NUMBER: MORPHO/5  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212)596-9000  
/ TELEFAX: (212)596-9090  
/ INFORMATION FOR SEQ ID NO: 36:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 120 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: <unknown>  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-490-324-36  
  
Query Match 80.6%; Score 541.5; DB 2; Length 120;  
Best Local Similarity 84.0%; Pred. No. 1.9e-44;  
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;  
  
QY 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY 60  
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY 60  
  
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120  
Db 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120  
  
QY 121 VTVSS 125  
Db 116 VTVSS 120  
  
RESULT 8  
US-09-490-324-59  
; Sequence 59, Application US/09490324  
; Patent No. 6828422  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,324  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US/09/025,769
/ FILING DATE: 18-FEB-1998
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/   NAME: James F. Haley, Jr., Esq.
/   REGISTRATION NUMBER: 27,794
/   REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (212)596-9000
/   TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 120 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-324-59

Query Match      80.6%; Score 541.5; DB 2; Length 120;
Best Local Similarity 84.0%; Pred. No. 1.9e-44;
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYCVRGFGYSYNYDYGGMDVWGQGT 120
Db 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYCVRGFGYSYNYDYGGMDVWGQGT 115
QY 121 VTVSS 125
Db 116 VTVSS 120

RESULT 9
US-09-025-769B-22
/ Sequence 22, Application US/09025769B
/ Patent No. 6300064
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ APPLICANT: Pack, Peter
/ APPLICANT: Ilag, Vic
/ APPLICANT: Ge, Liming
/ APPLICANT: Moroney, Simon
/ APPLICANT: Plueckthun, Andreas
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
/ STREET: 1251 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10021
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,769B
/ FILING DATE: 18-FEB-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 59:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 120 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: unknown
/   TOPOLOGY: linear
/

/
/ APPLICATION NUMBER: (212)596-9000
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 117 amino acids
/   TYPE: amino acid
/   STRANDEDNESS:
/   TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-025-769B-22

Query Match      78.6%; Score 528; DB 2; Length 117;
Best Local Similarity 82.5%; Pred. No. 3.5e-43;
Matches 104; Conservative 5; Mismatches 7; Indels 10; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYCVR-GFGYSYNYDYGGMDVWGQGT 119
Db 61 AQKFGQRTVMTDTSISTAYMELSLRSDDTAVYVCARDGDG-----GFDYWGQGT 111
QY 120 VTVSS 125
Db 112 VTVSS 117

RESULT 10
US-09-490-070A-22
/ Sequence 22, Application US/09490070A
/ Patent No. 6696248
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ APPLICANT: Pack, Peter
/ APPLICANT: Ilag, Vic
/ APPLICANT: Ge, Liming
/ APPLICANT: Moroney, Simon
/ APPLICANT: Plueckthun, Andreas
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
/             White & McAuliffe
/ STREET: 1666 K Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20006
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/490,070A
/ FILING DATE: 24-Jan-2000
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Colin G. Sandercock, Esq.
/ REGISTRATION NUMBER: 31,298
/ REFERENCE/DOCKET NUMBER: 37629-0005
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 912-2000
/ TELEFAX: (202) 912-2020
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 117 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: unknown
/   TOPOLOGY: linear
/
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Query Match 78.6%; Score 528; DB 2; Length 117;  
Best Local Similarity 82.5%; Pred. No. 3.5e-43;

QY 61 AOKFQGRVTMTDTSISTAYMELSSLSRSDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119  
 DB 61 AOKFQGRVTMTDTSISTAYMELSSLSRSDTAIYYCARDGDG-----GFDYWGQGT 111  
 QY 120 TVTVSS 125  
 DB 112 LTVSS 117

RESULT 13

US-09-859-053-28  
 ; Sequence 28, Application US/09859053  
 ; Patent No. 6803039  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tezuka, Takashi  
 ; APPLICANT: Tezuka, Katsunari  
 ; APPLICANT: Hori, No. 6803039uaki  
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
 ; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND  
 ; FILE REFERENCE: 06501-079001  
 ; CURRENT APPLICATION NUMBER: US/09/859,053  
 ; CURRENT FILING DATE: 2001-05-16  
 ; PRIOR APPLICATION NUMBER: JP 2001-99508  
 ; PRIOR FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: JP 2000-147116  
 ; PRIOR FILING DATE: 2000-05-18  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 28  
 ; LENGTH: 470  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-859-053-28

Query Match 78.3%; Score 526; DB 2; Length 470;  
 Best Local Similarity 79.2%; Pred. No. 2.6e-42;  
 Matches 99; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVOLVOSGAEVKPKGASVKVSKASGYTFTSYDINNVRQATGCGLEWMGWINPNSGNTDY 60  
 DB 20 QVOLVOSGAEVKPKGASVKVSKASGYTFTGYMHWVRQAPGCGLEWMGWINPHSGGNTY 79  
 QY 61 AOKFQGRVTMTDTSISTAYMELSSLSRSDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120  
 DB 80 AOKFQGRVTMTDTSISTAYMELSSLSRSDTAIYYCARDTYYDSSGYYHDAFDWQGT 139

RESULT 14

US-09-199-149-3  
 ; Sequence 3, Application US/09199149  
 ; Patent No. 6160099  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jonak, Zdenka L.  
 ; APPLICANT: Taylor, Alexander H.  
 ; APPLICANT: Trulli Jr., Stephen H.  
 ; APPLICANT: Johanson, Kyung O.  
 ; TITLE OF INVENTION: Humanized Monoclonal Antibodies  
 ; FILE REFERENCE: P50860  
 ; CURRENT APPLICATION NUMBER: US/09/199,149  
 ; CURRENT FILING DATE: 1998-11-24  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 125  
 ; TYPE: PRT  
 ; ORGANISM: Kabat VH subgroup I  
 US-09-199-149-3

Query Match 76.3%; Score 513; DB 2; Length 125;  
 Best Local Similarity 80.6%; Pred. No. 1e-41;  
 Matches 104; Conservative 8; Mismatches 9; Indels 8; Gaps 5;  
 QY 1 QVOLVOSGAEVKPKGASVKVSKASGYTFTSYDINNVRQATGCGLEWMGWINPNSGNTDY 60  
 DB 1 QVOLVOSGAEVKPKGASVKVSKASGYTFTSYAISWVRQAPGCGLEWMGWINP-GGDTNY 59  
 QY 61 AOKFQGRVTMTDTSISTAYMELSSLSRSDTAIYYCVR-GFGYS---YNDYYGMDVWG 116  
 DB 60 AOKFQGRVTITADTSTAYMELSSLSRSDTAIYYCARPGYGGCGYGY-WYWG--VWG 116  
 QY 117 QGTVTVSS 125  
 DB 117 QGTVTVSS 125

RESULT 15

US-08-202-047-22  
 ; Sequence 22, Application US/08202047  
 ; Patent No. 5800815  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHESNUT, Robert W.  
 ; APPLICANT: POLLEY, Margaret J.  
 ; APPLICANT: PAULSON, James C.  
 ; APPLICANT: JONES, S. Tarran  
 ; APPLICANT: SALDANHA, Jose W.  
 ; APPLICANT: BENDIG, Mary M.  
 ; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses  
 ; NUMBER OF SEQUENCES: 45  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/202,047  
 ; FILING DATE: 25-FEB-1994  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M.  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 14137-77  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-326-2400  
 ; TELEFAX: 415-326-2422  
 ; INFORMATION FOR SEQ ID NO: 22:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 128 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FEATURE:  
 ; NAME/KEY: Protein  
 ; LOCATION: 1..128  
 ; OTHER INFORMATION: /label= HUMAN\_I  
 US-08-202-047-22

Query Match 76.0%; Score 510.5; DB 1; Length 128;  
 Best Local Similarity 77.9%; Pred. No. 1.8e-41;  
 Matches 102; Conservative 7; Mismatches 13; Indels 9; Gaps 3;  
 QY 1 QVOLVOSGAEVKPKGASVKVSKASGYTFTSYDINNVRQATGCGLEWMGWINP-NSGNTD 59  
 DB 1 QVOLVOSGAEVKPKGASVKVSKASGYTFTSYAISWVRQAPGCGLEWMGWINPYGNDTN 60



Qy	60	YAKFQGRVTWTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYS-----YNYDYYYGMDV	114
Db	61	YAKFQGRVTITADTSTSTAYMELSSLRSEDTAIYYCARAPCGSGGGCYRGDYF---DY	117
Qy	115	WQGGTTTVTVSS	125
Db	118	WQGGTLTVTVSS	128

Search completed: April 25, 2007, 04:08:31  
Job time : 16.7133 secs

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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 46 Seconds  
(without alignments)  
1251.741 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....YDYYGMDVWGQGTITVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	672	100.0	125	4	US-10-041-860-48
2	672	100.0	125	4	US-10-041-860-200
3	672	100.0	125	4	US-10-041-860-237
4	672	100.0	125	4	US-10-041-860-372
5	672	100.0	125	4	US-10-041-860-383-2
6	638	94.9	125	4	US-10-041-860-38
7	638	94.9	125	4	US-10-041-860-203
8	638	94.9	125	4	US-10-041-860-240
9	638	94.9	125	4	US-10-041-860-343
10	638	94.9	125	4	US-10-041-860-354
11	593.5	88.3	126	4	US-10-041-860-19
12	593.5	88.3	126	4	US-10-041-860-201
13	593.5	88.3	126	4	US-10-041-860-208
14	593.5	88.3	126	4	US-10-041-860-218
15	579.5	86.2	125	4	US-10-041-860-238
16	575.5	85.6	126	4	US-10-041-860-40
17	575.5	85.6	126	4	US-10-041-860-204
18	575.5	85.6	126	4	US-10-041-860-241
19	575.5	85.6	126	4	US-10-041-860-349
20	575.5	85.6	126	4	US-10-041-860-358
21	572	85.1	127	4	US-10-041-860-44
22	572	85.1	127	4	US-10-041-860-205
23	572	85.1	127	4	US-10-041-860-242
24	572	85.1	127	4	US-10-041-860-360
25	572	85.1	127	4	US-10-041-860-66
26	567.5	84.4	126	4	US-10-041-860-21
27	567.5	84.4	126	4	US-10-041-860-199

## ALIGNMENTS

### RESULT 1

US-10-041-860-48  
; Sequence 48, Application US/10041860  
; Publication No. US20030157109A1

GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadi

; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: ARGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041,860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 48

; LENGTH: 125

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-041-860-48

Query Match 100.0%; Score 672; DB 4; Length 125;  
Best Local Similarity 100.0%; Pred. No. 9.5e-54;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY	60
Db	1	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWGWINPNSGNTDY	60
Qy	61	AQKFGQRTVTRDTSISTAYMELSSLSSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT	120
Db	61	AQKFGQRTVTRDTSISTAYMELSSLSSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT	120
Qy	121	VTVSS 125	
Db	121	VTVSS 125	

### RESULT 2

US-10-041-860-200

; Sequence 200, Application US/10041860

; Publication No. US20030157109A1

GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

121 VTVSS 125

```
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-237

Query Match      100.0%; Score 672; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.5e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 3
US-10-041-860-237
; Sequence 237, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-237

Query Match      100.0%; Score 672; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.5e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 4
US-10-041-860-372
; Sequence 372, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-372

Query Match      100.0%; Score 672; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.5e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 5
US-10-665-383-2
; Sequence 2, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-2
```



```

RESULT 9
US-10-041-860-343
; Sequence 343, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-343

Query Match      94.9%; Score 638; DB 4; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.2e-50;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGY 60

QY 61 AQKFGQGRVTMTDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQGRVTMTDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYGGMDVWGQGT 120

QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 11
US-10-041-860-19
; Sequence 19, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-19

Query Match      88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.5e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGY 60

QY 61 AQKFGQGRVTMTDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNYDYGGMDVWGQGT 119
DB 61 AQKFGQGRVTMTDTSISTAYMELSSLRSEDTAIYYCAREGIAVAGTYYYYYGGMDVWGQGT 120

QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 12
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-54

Query Match      94.9%; Score 638; DB 4; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.2e-50;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGY 60

QY 61 AQKFGQGRVTMTDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQGRVTMTDTSISTAYMELSSLRSEDTAIYYCARGSGYSYGYDYGGMDVWGQGT 120

QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 10
US-10-665-383-54
; Sequence 54, Application US/10665383
; Publication No. US20040141569A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-54
```

```
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

Query Match      88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.5e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
DB 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 120

QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 13
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288

Query Match      88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.5e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
DB 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 120

QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 14
US-10-665-383-18
; Sequence 18, Application US/10665383
; Publication No. US20040141969A1

; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRochele, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-18

Query Match      88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.5e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
DB 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 120

QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 15
US-10-041-860-238
; Sequence 238, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-238

Query Match      86.2%; Score 579.5; DB 4; Length 125;
Best Local Similarity 89.4%; Pred. No. 2.7e-45;
Matches 110; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 LVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAQK 63
DB 3 LVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGYAQK 62

QY 64 FQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 122
```



GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:23:02 ; Search time 48 Seconds  
(without alignments)  
533.620 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVOLVQSGAEVKKPGASVKV.....YDYRYGMDVWGQGTITVTSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 947558 seqs, 205760075 residues

Total number of hits satisfying chosen parameters: 947558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	672	100.0	125	7 US-11-109-181-48	Sequence 48, Appl
2	672	100.0	125	7 US-11-109-181-200	Sequence 200, App
3	672	100.0	125	7 US-11-109-181-237	Sequence 237, App
4	672	100.0	125	7 US-11-109-181-372	Sequence 372, App
5	638	94.9	125	7 US-11-109-181-38	Sequence 38, Appl
6	638	94.9	125	7 US-11-109-181-203	Sequence 203, App
7	638	94.9	125	7 US-11-109-181-240	Sequence 240, App
8	638	94.9	125	7 US-11-109-181-343	Sequence 343, App
9	599	89.1	126	7 US-11-433-924-94	Sequence 94, Appl
10	593.5	88.3	126	7 US-11-109-181-19	Sequence 19, Appl
11	593.5	88.3	126	7 US-11-109-181-201	Sequence 201, App
12	593.5	88.3	126	7 US-11-109-181-288	Sequence 288, App
13	579.5	86.2	125	7 US-11-109-181-238	Sequence 238, App
14	576.5	85.8	122	7 US-11-433-924-234	Sequence 234, App
15	575.5	85.6	126	7 US-11-109-181-40	Sequence 40, Appl
16	575.5	85.6	126	7 US-11-109-181-204	Sequence 204, App
17	575.5	85.6	126	7 US-11-109-181-241	Sequence 241, App
18	575.5	85.6	126	7 US-11-109-181-349	Sequence 349, App
19	572	85.1	127	7 US-11-109-181-44	Sequence 44, Appl
20	572	85.1	127	7 US-11-109-181-205	Sequence 205, App
21	572	85.1	127	7 US-11-109-181-242	Sequence 242, App
22	572	85.1	127	7 US-11-109-181-360	Sequence 360, App
23	570	84.8	126	7 US-11-311-939-425	Sequence 425, App
24	570	84.8	126	7 US-11-311-939-429	Sequence 429, App
25	567.5	84.4	126	7 US-11-109-181-21	Sequence 21, Appl

#### ALIGNMENTS

##### RESULT 1

US-11-109-181-48  
; Sequence 48, Application US/11109181  
; Publication No. US20060293506A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezaheh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: ABGENIX.051A  
; CURRENT APPLICATION NUMBER: US/11/109,181  
; CURRENT FILING DATE: 2005-04-18  
; PRIOR APPLICATION NUMBER: US/10/041,860  
; PRIOR FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-11-109-181-48

Query Match 100.0%; Score 672; DB 7; Length 125;  
Best Local Similarity 100.0%; Pred. No. 7.9e-56;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QVOLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY	60
DB	1	QVOLVQSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY	60
QY	61	AKQFQGRVTMTRTSISTATMELSSLRSEDTAIYVCVRGFGYSNYDYGVMDVWGQGT	120
DB	61	AKQFQGRVTMTRTSISTATMELSSLRSEDTAIYVCVRGFGYSNYDYGVMDVWGQGT	120
QY	121	VTVSS 125	
DB	121	VTVSS 125	

##### RESULT 2

US-11-109-181-200  
; Sequence 200, Application US/11109181



```
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-200

Query Match      100.0%; Score 672; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 7.9e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATQGQLEWGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATQGQLEWGWINPNSGNTDY 60

QY 61 AOKFQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AOKFQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120

QY 121 VTSS 125
DB 121 VTSS 125

RESULT 4
US-11-109-181-372
; Sequence 372, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-372

Query Match      100.0%; Score 672; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 7.9e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATQGQLEWGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINVRQATQGQLEWGWINPNSGNTDY 60

QY 61 AOKFQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AOKFQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120

QY 121 VTSS 125
DB 121 VTSS 125

RESULT 5
US-11-109-181-38
; Sequence 38, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
```

```
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-38

Query Match          94.9%; Score 638; DB 7; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.3e-52;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 6
US-11-109-181-203
; Sequence 203, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-203

Query Match          94.9%; Score 638; DB 7; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.3e-52;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 7
US-11-109-181-240
; Sequence 240, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-240

Query Match          94.9%; Score 638; DB 7; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.3e-52;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 8
US-11-109-181-343
; Sequence 343, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-343

Query Match          94.9%; Score 638; DB 7; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.3e-52;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125
```

```

; ORGANISM: homo sapiens
US-11-109-181-343

Query Match      94.9%; Score 638; DB 7; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.3e-52;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVOLVQSGAEVKKPGASVKASKASYFTTSDYDINWVRQATGQGLEWMGWNPNSGNTDY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVOLVQSGAEVKKPGASVKASKASYFTTSDYDINWVRQATGQGLEWMGWNPNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 AQKFGQRTVMTTRDTSISTAYMELSLRSRSDTAIYYCVRGFGSYNYYGMDVWGQTT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKFGQRTVMTTRNTSISTAYMELSLRSRSDTAIYYCARGSGSYGYDYIYGMDVWGQTT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 TVTVSS 125
    |||||
Db 121 TVTVSS 125
    |||||

RESULT 9
US-11-433-924-94
; Sequence 94, Application US/11433924
; Publication No. US20060286112A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Aimee
; APPLICANT: Poord, Orit
; APPLICANT: Belouski, Shelley Sims
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
; TITLE OF INVENTION: OTHER DISORDERS
; FILE REFERENCE: ABGENIX.120A
; CURRENT APPLICATION NUMBER: US/11/433,924
; CURRENT FILING DATE: 2006-05-12
; PRIOR APPLICATION NUMBER: US 60/681,846
; PRIOR FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-433-924-94

Query Match      89.1%; Score 599; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 5.9e-49;
Matches 113; Conservative 5; Mismatches 6; Indels 2; Gaps 1;

Qy 1 QVOLVQSGAEVKKPGASVKASKASYFTTSDYDINWVRQATGQGLEWMGWNPNSGNTDY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVOLVQSGAEVKKPGASVKASKASYFTTSDYDINWVRQATGQGLEWMGWNPNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 AQKFGQRTVMTTRDTSISTAYMELSLRSRSDTAIYYCVRGFGVSV--NYDYIYGMDVWGQ 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKFGQRTVMTTRNTSISTAYMELSLRSRSDTAIYYCARGYSSSWYRGYIYGMDVWGQ 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 119 TVTVSS 124
    |||||
Db 121 TVTVSS 126
    |||||

RESULT 10
US-11-109-181-19
; Sequence 19, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi

```

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; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR APPLICATION NUMBER: 2005-04-18
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-19

Query Match      88.3%; Score 593.5; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 2e-48;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVOLVQSGAEVKKPGASVKASKASYFTTSDYDINWVRQATGQGLEWMGWNPNSGNTDY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVOLVQSGAEVKKPGASVKASKASYFTTSDYDINWVRQATGQGLEWMGWNPNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 AQKFGQRTVMTTRDTSISTAYMELSLRSRSDTAIYYCVR-GFGYSYNYDYIYGMDVWGQGT 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKFGQRTVMTTRNTSISTAYMELSLRSRSDTAIYYCAREGIAVAGTYYYYYIYGMDVWGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 120 TVTVSS 125
    |||||
Db 121 TVTVSS 126
    |||||

RESULT 11
US-11-109-181-201
; Sequence 201, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-201

Query Match      88.3%; Score 593.5; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 2e-48;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVOLVQSGAEVKKPGASVKASKASYFTTSDYDINWVRQATGQGLEWMGWNPNSGNTDY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVOLVQSGAEVKKPGASVKASKASYFTTSDYDINWVRQATGQGLEWMGWNPNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 AQKFGQRTVMTTRDTSISTAYMELSLRSRSDTAIYYCVR-GFGYSYNYDYIYGMDVWGQGT 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKFGQRTVMTTRNTSISTAYMELSLRSRSDTAIYYCAREGIAVAGTYYYYYIYGMDVWGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 120 TVTVSS 125
    |||||
Db 121 TVTVSS 126
    |||||

```



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; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-40

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Query Match      85.6%; Score 575.5; DB 7; Length 126;
Best Local Similarity 87.3%; Pred.No. 9.7e-47;
Matches 110; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY      1 QVQLVQSGAEVKKPKASVKVSKASGYTFTSYDINWVRQATQGGLEWGMWINPNSGNTDY 60
Db      1 QVQLVQSGAEVKKPKASVKVSKASGYTFTSYDINWVRQATQGGLEWGMWINPNSGNTDY 60

QY      61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYN-YDYIYGMQVWGQGT 119
Db      61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYN-YDYIYGMQVWGQGT 120

QY      120 TTVTVSS 125
Db      121 TTVTVSS 126

```

Search completed: April 25, 2007, 04:27:43  
Job time : 48.1992 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 94 Seconds  
(without alignments)  
564.248 Million cell updates/sec

Title: US-10-665-383-4  
Perfect score: 558  
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQYGSPPCSFGQTKLEIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*  
10: Geneseqp2006s.\*  
11: Geneseqp2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	108	7 ADK18625	Adk18625 Anti-huma
2	558	100.0	108	7 ADK18951	Adk18951 Anti-huma
3	558	100.0	108	7 ADK18835	Adk18835 Anti-huma
4	558	100.0	108	7 ADK18801	Adk18801 Anti-huma
5	558	100.0	108	8 ADL25394	Adl25394 Human mAb
6	543	97.3	109	10 AEF73695	Aef73695 Human IL-
7	543	97.3	236	10 AEF73710	Aef73710 Human IL-
8	535	95.9	108	9 ADY26769	Ady26769 Anti-NGF-
9	535	95.9	108	9 ADY26816	Ady26816 Human ant
10	535	95.9	128	9 AD257709	Ad257709 Germline
11	535	95.9	129	2 AAR38672	Aar38672 vK325-Jk2
12	533	95.5	108	7 ADP03986	Adp03986 Murine-ex
13	533	95.5	120	10 AEH89253	Aeh89253 Anti-VEGF
14	533	95.5	130	6 ABJ36930	Abj36930 Anti-CD40
15	533	95.5	130	10 AEG95253	Aeg95253 Human imm
16	533	95.5	140	10 AEH89279	Aeh89279 Anti-VEGF
17	533	95.5	384	4 AAM24101	Aam24101 Human EST
18	532	95.3	108	8 ADQ16703	Adq16703 Modified
19	532	95.3	108	9 ADV44439	Adv44439 pAX116 va
20	532	95.3	108	9 AEB12911	Aeb12911 Antibody
21	532	95.3	108	9 AEC81271	Aec81271 Human mon
22	532	95.3	108	9 AEC81269	Aec81269 Human mon

23	532	95.3	108	9 AEC81267	Aec81267 Human mon
24	532	95.3	108	10 AEF81808	Aef81808 Human ant
25	532	95.3	108	10 AEF81806	Aef81806 Human ant
26	532	95.3	108	10 AEF81804	Aef81804 Human ant
27	532	95.3	109	8 ADP46971	Adp46971 Murine li
28	532	95.3	109	10 AEF65167	Aef65167 Anti-Ang-
29	532	95.3	112	9 ADV44477	Adv44477 Anti-teta
30	532	95.3	115	10 AEE03759	Aee03759 Antibody
31	532	95.3	120	7 ADD40551	Add40551 3E1/4G11
32	532	95.3	130	9 AEB12948	Aeb12948 Antibody
33	532	95.3	215	8 ADQ16702	Adq16702 Modified
34	532	95.3	215	9 ADV44438	Adv44438 pAX116 va
35	532	95.3	215	9 AEB12910	Aeb12910 Antibody
36	532	95.3	239	9 ADV44458	Adv44458 Anti-teta
37	532	95.3	239	9 AEB12929	Aeb12929 Antibody
38	531	95.2	108	9 ADZ42030	Adz42030 Ig L chai
39	531	95.2	108	9 ADZ42032	Adz42032 Ig L chai
40	531	95.2	108	9 ADZ42034	Adz42034 Ig L chai
41	531	95.2	108	9 AEA89845	Aea89845 Anti-IFN
42	530	95.0	384	4 AAU14462	Aau14462 Human nov
43	530	95.0	384	4 AAU14463	Aau14463 Human nov
44	530	95.0	384	4 AAU14461	Aau14461 Human nov
45	530	95.0	384	4 AAU14464	Aau14464 Human nov

## ALIGNMENTS

RESULT 1  
ADK18625  
ID ADK18625 standard; protein; 108 AA.  
AC ADK18625;  
XX  
DT 06-MAY-2004 (first entry)  
DE Anti-human PDGF-D antibody light chain protein sequence.  
XX  
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.  
OS Homo sapiens.  
XX  
XX WC2003057857-A2.  
PN  
PD 17-JUL-2003.  
XX  
XX 06-JAN-2003; 2003WO-US000398.  
XX  
XX 07-JAN-2002; 2002US-00041860.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
Bezabeh B;  
XX  
XX WPI; 2003-587119/55.  
XX  
XX New human monoclonal antibody that binds to platelet-derived growth  
factor-D (PDGF-D), useful for treating chronic and recurrent human  
diseases, such as inflammation, autoimmunity and cancer.  
XX  
XX Disclosure; SEQ ID NO 49; 255pp; English.

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 558; DB 7; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-35;  
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGAPRLLIYATSSRATGIP 60  
 |||||  
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGAPRLLIYATSSRATGIP 60  
 |||||

QY 61 DRFSGSGGTDTLTISRLEPEDPAVYVYCOQYGGSSPCSPGQGTKEIK 108  
 |||||  
 DB 61 DRFSGSGGTDTLTISRLEPEDPAVYVYCOQYGGSSPCSPGQGTKEIK 108  
 |||||

RESULT 2

ADK18951  
 ID ADK18951 standard; protein; 108 AA.  
 AC ADK18951;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Anti-human PDGF-D antibody protein related sequence #177.  
 XX  
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057857-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 06-JAN-2003; 2003WO-US000398.  
 XX  
 PR 07-JAN-2002; 2002US-00041860.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX  
 DR WPI; 2003-587119/55.  
 XX  
 PT New human monoclonal antibody that binds to platelet-derived growth  
 factor-D (PDGF-D), useful for treating chronic and recurrent human  
 diseases, such as inflammation, autoimmunity and cancer.  
 XX  
 PS Disclosure; SEQ ID NO 375; 255pp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody that binds to  
 platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 treating chronic and recurrent human diseases, such as inflammation,  
 autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 useful for modulating collagen formation, and for staging various  
 cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 generated using an active protein fragment of the gene product from the  
 clone 30664188.0.99 arising in the conditioned medium obtained when  
 HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 sequence corresponds to a protein used in the invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 558; DB 7; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-35;  
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGAPRLLIYATSSRATGIP 60  
 |||||  
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGAPRLLIYATSSRATGIP 60  
 |||||

QY 61 DRFSGSGGTDTLTISRLEPEDPAVYVYCOQYGGSSPCSPGQGTKEIK 108  
 |||||  
 DB 61 DRFSGSGGTDTLTISRLEPEDPAVYVYCOQYGGSSPCSPGQGTKEIK 108  
 |||||

DB 61 DRFSGSGGTDTLTISRLEPEDPAVYVYCOQYGGSSPCSPGQGTKEIK 108  
 |||||

RESULT 3

ADK18835  
 ID ADK18835 standard; protein; 108 AA.  
 AC ADK18835;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Anti-human PDGF-D antibody protein related sequence #61.  
 XX  
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057857-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 06-JAN-2003; 2003WO-US000398.  
 XX  
 PR 07-JAN-2002; 2002US-00041860.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX  
 DR WPI; 2003-587119/55.  
 XX  
 PT New human monoclonal antibody that binds to platelet-derived growth  
 factor-D (PDGF-D), useful for treating chronic and recurrent human  
 diseases, such as inflammation, autoimmunity and cancer.  
 XX  
 PS Disclosure; SEQ ID NO 259; 255pp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody that binds to  
 platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 treating chronic and recurrent human diseases, such as inflammation,  
 autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 useful for modulating collagen formation, and for staging various  
 cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 generated using an active protein fragment of the gene product from the  
 clone 30664188.0.99 arising in the conditioned medium obtained when  
 HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 sequence corresponds to a protein used in the invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 558; DB 7; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-35;  
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGAPRLLIYATSSRATGIP 60  
 |||||  
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGAPRLLIYATSSRATGIP 60  
 |||||

QY 61 DRFSGSGGTDTLTISRLEPEDPAVYVYCOQYGGSSPCSPGQGTKEIK 108  
 |||||  
 DB 61 DRFSGSGGTDTLTISRLEPEDPAVYVYCOQYGGSSPCSPGQGTKEIK 108  
 |||||

RESULT 4

ADK18801  
 ID ADK18801 standard; protein; 108 AA.  
 AC ADK18801;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX

DE Anti-human PDGF-D antibody protein related sequence #27.

XX antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX Homo sapiens.

XX WO2003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;

XX Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth

XX factor-D (PDGF-D), useful for treating chronic and recurrent human

XX diseases, such as inflammation, autoimmunity and cancer.

XX Disclosure; SEQ ID NO 225; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to

XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for

XX treating chronic and recurrent human diseases, such as inflammation,

XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are

XX useful for modulating collagen formation, and for staging various

XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were

XX generated using an active protein fragment of the gene product from the

XX clone 30664188.0.99 arising in the conditioned medium obtained when

XX HBK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This

XX sequence corresponds to a protein used in the invention.

XX Sequence 108 AA;

XX Query Match 100.0%; Score 558; DB 7; Length 108;

XX Best Local Similarity 100.0%; Pred. No. 4.6e-35;

XX Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

XX 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

XX 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYSGSPCSFGQGTGLEIK 108

XX 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYSGSPCSFGQGTGLEIK 108

XX RESULT 5

XX ADL25394

XX ID ADL25394 standard; protein; 108 AA.

XX AC ADL25394;

XX 17-JUN-2004 (first entry)

XX Human mAb 6.4 light chain variable region protein SEQ ID NO:4.

XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;

XX nephritis; mesangial cell proliferation inhibition;

XX mesangial proliferative glomerulonephritis; nephrotropic;

XX antiinflammatory; dermatological; immunosuppressive; antidiabetic;

XX Gene therapy; human; monoclonal antibody; mAb.

XX Homo sapiens.

XX OS WO2004024098-A2.

XX PN

XX

PD 25-MAR-2004.

XX 16-SEP-2003; 2003WO-US029414.

XX 16-SEP-2002; 2002US-0411137P.

XX (ABGE-) ABGENIX INC.

XX (CURA-) CURAGEN CORP.

XX Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;

XX WPI; 2004-269881/25.

XX N-PSDB; ADL25393.

XX Use of an antibody or its binding fragment that binds platelet derived

XX growth factor-DD (PDGF-DD) for preparing a medicament for treating

XX nephritis.

XX Disclosure; SEQ ID NO 4; 115pp; English.

XX The present invention describes an antibody or its binding fragment that

XX binds platelet derived growth factor-DD (PDGF-DD), where the antibody is

XX useful in preparing a medicament for treating nephritis. Also described:

XX (1) a method of detecting nephritis; (2) a method of treating nephritis;

XX (3) a method of inhibiting mesangial cell proliferation; and (4) a method

XX of treating mesangial proliferative glomerulonephritis. The antibody has

XX nephrotropic, antiinflammatory, dermatological, immunosuppressive and

XX antidiabetic activities, and can be used in gene therapy. The antibody or

XX its binding fragment, that binds PDGF-DD, can be used in preparing a

XX medicament for treating nephritis and related disorders, e.g., mesangial

XX proliferative glomerulonephritis. The present sequence represents a human

XX monoclonal antibody (mAb) variable region sequence, which is used in the

XX exemplification of the present invention.

XX SQ Sequence 108 AA;

XX Query Match 100.0%; Score 558; DB 8; Length 108;

XX Best Local Similarity 100.0%; Pred. No. 4.6e-35;

XX Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

XX 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

XX 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYSGSPCSFGQGTGLEIK 108

XX 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYSGSPCSFGQGTGLEIK 108

XX RESULT 6

XX AEF73695

XX ID AEF73695 standard; protein; 109 AA.

XX AC AEF73695;

XX 06-APR-2006 (first entry)

XX Human IL-17 antibody AIN457 light chain variable region.

XX Interleukin-17 antagonist; antibody production; antibody therapy;

XX osteoarthritis; rheumatoid arthritis; osteoporosis; inflammation;

XX antiarthritic; antirheumatic; osteopathic; antiinflammatory;

XX musculoskeletal disease; immune disorder; inflammation; degeneration;

XX endocrine disease; light chain variable region.

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers

XX FT Region 24..35

XX FT /label= L-CDR1

XX FT Region 51..57

XX FT /label= L-CDR2

XX FT Region 90..98



/label= L-CDR3

FT XX WO2006013107-A1.  
 PN XX  
 XX XX  
 PD 09-FEB-2006.  
 XX XX  
 PF 04-AUG-2005; 2005WO-EP008470.  
 PR XX  
 PR 05-AUG-2004; 2004GB-00017487.  
 XX XX  
 XX (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS PHARMA GMBH.  
 XX XX  
 PI Di Padova FE, Gram H, Hofstetter H, Jeschke M, Rondeau J;  
 PI Van Den Berg W;  
 XX XX  
 DR WPI; 2006-145760/15.  
 DR N-PSDB; AEF73694.  
 XX XX  
 PT Novel interleukin-17 binding molecule capable of inhibiting human IL-17  
 PT activity and IL-6 production induced by human-IL-17 in human dermal  
 PT fibroblasts, useful for treating IL-mediated diseases e.g.  
 PT osteoarthritis.  
 XX XX  
 PS Claim 5; SEQ ID NO 10; 76pp; English.  
 XX XX  
 CC The present invention relates to interleukin-17 (IL-17) antagonistic  
 CC antibodies suitable for use in the treatment of IL-17 mediated diseases  
 CC and disorders. A claimed IL-17 binding molecule is capable of inhibiting  
 CC the activity of 1 nM human IL-17 at a concentration of less than 5 nM by  
 CC 50%, the activity being measured on interleukin-6 production induced by  
 CC human IL-17 in human dermal fibroblasts. The IL-17 binding molecule  
 CC comprises: a heavy chain variable region (VH) comprising complementarity  
 CC determining regions CDR1, CDR2 and CDR3 AEF73686-AEF73688 or CDR1-x, CDR2  
 CC -x and CDR3-x AEF73696-AEF73698 from anti-human IL-17 antibody AIN457;  
 CC and a light chain variable region (LH) comprising CDR1', CDR2' and CDR3',  
 CC AEF73689-AEF73691 from AIN457. The IL-17 binding molecule is preferably a  
 CC human antibody. It preferably comprises at least one antigen binding site  
 CC comprising a first domain having amino acid sequence homology to the  
 CC AIN457 VH region AEF73693 and a second domain having amino acid sequence  
 CC homology to the AIN457 VL region AEF73695. Also provided are a DNA  
 CC construct encoding the IL-17 binding molecules of the invention, an  
 CC expression vector comprising the DNA construct, and a method of producing  
 CC an IL-17 binding molecule by culturing a transformed host cell line. The  
 CC IL-17 binding molecule is used to manufacture a medicament for the  
 CC treatment of an IL-17 mediated disease or disorder, especially  
 CC osteoarthritis, rheumatoid arthritis, osteoporosis and other inflammatory  
 CC arthritides. In an example from the invention, transgenic mouse 27340,  
 CC which is engineered to express the human Igg/kappa repertoire instead of  
 CC the murine immunoglobulin repertoire, was used to generate antibodies to  
 CC human IL-17. B-cells from these mice were immortalized by standard  
 CC hybridoma technology and murine hybridoma cells were obtained which  
 CC secreted the human IgG1/kappa antibody AIN457. The present sequence is  
 CC the amino acid sequence of AIN457 VL.  
 XX XX  
 SQ Sequence 109 AA;  
 Query Match 97.3%; Score 543; DB 10; Length 109;  
 Best Local Similarity 96.3%; Pred. No. 6.4e-34;  
 Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYYATSSRATGIP 60  
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYYATSSRATGIP 60  
 QY 61 DRFSGSGSTDTLTISRLEPEDFAVYYCQQYGGSPCSFGQGTKLIK 108  
 DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYYCQQYGGSPCSFGQGTKLIK 108  
 RESULT 7  
 AEF73710  
 ID AEF73710 standard; protein; 236 AA.

XX AEF73710;  
 AC 06-APR-2006 (first entry)  
 DT Human IL-17 antibody AIN457 light chain.  
 XX XX  
 DE Interleukin-17 antagonist; antibody production; antibody therapy;  
 KW osteoarthritis; rheumatoid arthritis; osteoporosis; inflammation;  
 KW osteoarthritic; antirheumatic; osteopathic; antiinflammatory;  
 KW musculoskeletal disease; immune disorder; inflammation; degeneration;  
 KW endocrine disease; light chain.  
 XX OS Homo sapiens.  
 XX XX  
 PH Key Location/Qualifiers  
 FT Region 45..56  
 FT /label= L-CDR1  
 FT Region 72..76  
 FT /label= L-CDR2  
 FT Region 111..119  
 FT /label= L-CDR3  
 XX XX  
 PN WO2006013107-A1.  
 XX XX  
 PD 09-FEB-2006.  
 XX XX  
 PF 04-AUG-2005; 2005WO-EP008470.  
 XX XX  
 PR 05-AUG-2004; 2004GB-00017487.  
 XX XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS PHARMA GMBH.  
 XX XX  
 PI Di Padova FE, Gram H, Hofstetter H, Jeschke M, Rondeau J;  
 PI Van Den Berg W;  
 XX XX  
 DR WPI; 2006-145760/15.  
 XX XX  
 PT Novel interleukin-17 binding molecule capable of inhibiting human IL-17  
 PT activity and IL-6 production induced by human-IL-17 in human dermal  
 PT fibroblasts, useful for treating IL-mediated diseases e.g.  
 PT osteoarthritis.  
 XX XX  
 PS Example 3; Page 43-44; 76pp; English.  
 XX XX  
 CC The present invention relates to interleukin-17 (IL-17) antagonistic  
 CC antibodies suitable for use in the treatment of IL-17 mediated diseases  
 CC and disorders. A claimed IL-17 binding molecule is capable of inhibiting  
 CC the activity of 1 nM human IL-17 at a concentration of less than 5 nM by  
 CC 50%, the activity being measured on interleukin-6 production induced by  
 CC human IL-17 in human dermal fibroblasts. The IL-17 binding molecule  
 CC comprises: a heavy chain variable region (VH) comprising complementarity  
 CC determining regions CDR1, CDR2 and CDR3 AEF73686-AEF73688 or CDR1-x, CDR2  
 CC -x and CDR3-x AEF73696-AEF73698 from anti-human IL-17 antibody AIN457;  
 CC and a light chain variable region (LH) comprising CDR1', CDR2' and CDR3',  
 CC AEF73689-AEF73691 from AIN457. The IL-17 binding molecule is preferably a  
 CC human antibody. It preferably comprises at least one antigen binding site  
 CC comprising a first domain having amino acid sequence homology to the  
 CC AIN457 VH region AEF73693 and a second domain having amino acid sequence  
 CC homology to the AIN457 VL region AEF73695. Also provided are a DNA  
 CC construct encoding the IL-17 binding molecules of the invention, an  
 CC expression vector comprising the DNA construct, and a method of producing  
 CC an IL-17 binding molecule by culturing a transformed host cell line. The  
 CC IL-17 binding molecule is used to manufacture a medicament for the  
 CC treatment of an IL-17 mediated disease or disorder, especially  
 CC osteoarthritis, rheumatoid arthritis, osteoporosis and other inflammatory  
 CC arthritides. In an example from the invention, transgenic mouse 27340,  
 CC which is engineered to express the human Igg/kappa repertoire instead of  
 CC the murine immunoglobulin repertoire, was used to generate antibodies to  
 CC human IL-17. B-cells from these mice were immortalized by standard  
 CC hybridoma technology and murine hybridoma cells were obtained which  
 CC secreted the human IgG1/kappa antibody AIN457. The present sequence is  
 CC the amino acid sequence of AIN457 VL.

CC the amino acid sequence of AIN457 light chain.  
 XX Sequence 236 AA;  
 SQ

Query Match 97.3%; Score 543; DB 10; Length 236;  
 Best Local Similarity 96.3%; Pred. No. 1.3e-33;  
 Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSVLAWYQKPGQAPRLIIYATSSRATGIP 60  
 |||||  
 Db 22 EIVLTQSPGTLSPGERATLSCRASQSVSSVLAWYQKPGQAPRLIIYATSSRATGIP 81  
 |||||

Qy 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108  
 |||||  
 Db 82 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCTFGQGTLEIK 129  
 |||||

RESULT 8  
 ADY26769  
 ID ADY26769 standard; protein; 108 AA.  
 XX  
 AC ADY26769;  
 XX  
 DT 19-MAY-2005 (first entry)  
 XX  
 DE Anti-NGF-antibody light chain variable region SEQ ID NO 84.  
 XX  
 DE analgesic; gene therapy; antibody engineering; pharmaceutical; pain;  
 KW neurological disease; NGF; nerve growth factor;  
 KW light chain variable region.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005019266-A2.  
 XX  
 PD 03-MAR-2005.  
 XX  
 PF 15-JUL-2004; 2004WO-US022876.  
 XX  
 PR 15-JUL-2003; 2003US-0487431P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;  
 XX WPI; 2005-202606/21.  
 DR

New human anti-nerve growth factor (NGF) neutralizing antibodies useful  
 for manufacturing a medicament for treating painful disorders (e.g. acute  
 pain) or conditions associated with increased expression or sensitivity  
 to NGF.

Claim 33; SEQ ID NO 84; 190pp; English.

The invention describes an isolated human antibody that interacts with or  
 binds specifically to human nerve growth factor (NGF) and neutralize the  
 function of NGF. Also described are: methods of treating a condition  
 caused by increased expression of NGF or increased sensitivity to NGF in  
 a patient; methods for detecting NGF in a biological sample; an NGF  
 specific binding agent comprising any of the 59 amino acid sequences  
 comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the  
 specification, and where the binding agent can bind to NGF; a  
 pharmaceutical composition comprising a pharmaceutical carrier and a  
 therapeutic amount of the antibody or binding agent cited above; or a  
 medicament for treating a painful disorder or condition associated with  
 increased expression of NGF or increased sensitivity to NGF, the  
 medicament comprising a pharmaceutical amount of a monoclonal antibody or  
 salts of the monoclonal antibody or the fragment, where the monoclonal  
 antibody is at least one of the monoclonal antibody cited above, and a  
 pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or  
 polynucleotide that encodes the above antibody or binding agent; an  
 isolated cell line that produces the above antibody or binding agent; an

CC expression vector comprising the above polynucleotide; and a host cell  
 CC comprising the nucleic acid or expression vector. The composition  
 CC (including the antibody) and methods are useful for manufacturing a  
 CC medicament for treating a painful disorder (e.g. acute pain, dental pain,  
 CC or pain from trauma or cancer), or a condition associated with increased  
 CC expression of NGF or increased sensitivity to NGF. This is the amino acid  
 CC sequence of a human NGF antibody light chain variable region.  
 XX  
 SQ Sequence 108 AA;

Query Match 95.9%; Score 535; DB 9; Length 108;  
 Best Local Similarity 96.3%; Pred. No. 2.6e-33;  
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSVLAWYQKPGQAPRLIIYATSSRATGIP 60  
 |||||  
 Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSVLAWYQKPGQAPRLIIYATSSRATGIP 60  
 |||||

Qy 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108  
 |||||  
 Db 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPYTFGQGTLEIK 108  
 |||||

RESULT 9  
 ADY26816  
 ID ADY26816 standard; protein; 108 AA.  
 XX  
 AC ADY26816;  
 XX  
 DT 19-MAY-2005 (first entry)  
 XX  
 DE Human anti-NGF-antibody light chain SEQ ID NO 131.  
 XX  
 DE analgesic; gene therapy; antibody engineering; pharmaceutical; pain;  
 KW neurological disease; NGF; nerve growth factor; light chain.  
 KW  
 XX Homo sapiens.  
 XX  
 PN WO2005019266-A2.  
 XX  
 PD 03-MAR-2005.  
 XX  
 PF 15-JUL-2004; 2004WO-US022876.  
 XX  
 PR 15-JUL-2003; 2003US-0487431P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;  
 XX WPI; 2005-202606/21.  
 DR

New human anti-nerve growth factor (NGF) neutralizing antibodies useful  
 for manufacturing a medicament for treating painful disorders (e.g. acute  
 pain) or conditions associated with increased expression or sensitivity  
 to NGF.

Claim 33; SEQ ID NO 131; 190pp; English.

The invention describes an isolated human antibody that interacts with or  
 binds specifically to human nerve growth factor (NGF) and neutralize the  
 function of NGF. Also described are: methods of treating a condition  
 caused by increased expression of NGF or increased sensitivity to NGF in  
 a patient; methods for detecting NGF in a biological sample; an NGF  
 specific binding agent comprising any of the 59 amino acid sequences  
 comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the  
 specification, and where the binding agent can bind to NGF; a  
 pharmaceutical composition comprising a pharmaceutical carrier and a  
 therapeutic amount of the antibody or binding agent cited above; or a  
 medicament for treating a painful disorder or condition associated with  
 increased expression of NGF or increased sensitivity to NGF, the  
 medicament comprising a pharmaceutical amount of a monoclonal antibody or  
 its immunologically functional immunoglobulin fragment, or pharmaceutical

CC salts of the monoclonal antibody or the fragment, where the monoclonal  
 CC antibody is at least one of the monoclonal antibody cited above, and a  
 CC pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or  
 CC polynucleotide that encodes the above antibody or binding agent; an  
 CC isolated cell line that produces the above antibody or binding agent; an  
 CC expression vector comprising the above polynucleotide; and a host cell  
 CC comprising the nucleic acid or expression vector. The composition  
 CC (including the antibody) and methods are useful for manufacturing a  
 CC medicament for treating a painful disorder (e.g. acute pain, dental pain,  
 CC or pain from trauma or cancer), or a condition associated with increased  
 CC expression of NGF or increased sensitivity to NGF. This is the amino acid  
 CC sequence of a human NGF antibody light chain.

XX Sequence 108 AA;

Query Match 95.9%; Score 535; DB 9; Length 108;

Best Local Similarity 96.3%; Pred. No. 2.6e-33;

Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPSCSFQGQTKLEIK 108

DB 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPYTFQGQTKLEIK 108

RESULT 10

ID AD257709 standard; protein; 128 AA.

XX AD257709;

DT 30-JUN-2005 (first entry)

DE Germline antibody A27Vk3, Jk2 light chain protein.

XX antibody engineering; cytostatic; vulnery; vasotropic; cardiant;  
 KW monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer;  
 KW gastrointestinal ulcer; ischemia; transplant rejection;  
 KW myocardial infarction; reperfusion injury; restenosis; angioplasty;  
 KW vascular disease; cancer; retinopathy; endometriosis; arthritis;  
 KW Alzheimer's disease; tumor; glioblastoma; sarcoma; carcinoma; diagnosis;  
 KW antibody.

OS Homo sapiens.

XX GB2404660-A.

XX 09-FEB-2005.

PF 04-AUG-2004; 2004GB-00017384.

XX 04-AUG-2003; 2003US-0492432P.

XX (PFIZ ) PFIZER PROD INC.

PA (ABGE-) ABGENIX INC.

XX Michaud NR, Kajiji S, Borzillo G, Bedian V, Coleman K, Green LL;  
 PI Jia X;

XX WPI; 2005-145169/16.

XX Human monoclonal antibody or antigen-binding portion that specifically  
 PT binds to c-Met, useful for treating cancer by inhibiting c-Met or for  
 PT promoting tissue regeneration and wound healing by activating c-Met.

XX Example 2; SEQ ID NO 18; 128pp; English.

XX The invention relates to a human monoclonal antibody (I) or its antigen-  
 CC binding portion that specifically binds to c-Met, comprises a heavy chain  
 CC having a fully defined sequence (S1) of 13.3.2 heavy chain, where X2 is

CC lysine and X4 is threonine, and a light chain having a fully defined  
 CC sequence (S2) of 13.3.2 light chain, where X8 is threonine, where both  
 CC chains are without a signal sequence. All the sequences are fully defined  
 CC in the specification. (I) is useful for the manufacture of a medicament  
 CC for treating a hyperproliferative disorder in a subject, where the  
 CC antibody or its portion is a c-Met antagonist. (I) is useful for  
 CC manufacture of a medicament for promoting wound healing or tissue  
 CC regeneration in a subject, where the antibody, antigen-binding portion or  
 CC the composition activates c-Met. (I) which has a c-Met agonist activity  
 CC is useful in tissue regeneration or wound healing (skin ulcers or gastric  
 CC ulcers), or treating ischemia associated with kidney transplant  
 CC rejection, for attenuating toxicity associated with cyclosporin treatment  
 CC after transplant surgery, for treating myocardial infarction, cardiac  
 CC ischemia due to reperfusion injury, restenosis after angioplasty or  
 CC vascular diseases. (I) which has a c-Met antagonist activity is useful  
 CC for treating cancers of brain, lung, squamous cell, bladder, neck, liver,  
 CC prostate, etc., proliferative vitreoretinopathy, proliferative diabetic  
 CC retinopathy, endometriosis, and arthritis, for inhibiting plaque  
 CC formation in Alzheimer's disease, inhibiting cellular mitogenic  
 CC responses, or for treating tumor, glioblastoma, sarcoma, or carcinomas.  
 CC (I) is useful for detecting c-Met in a biological sample in vitro or in  
 CC vivo, thus useful for diagnosing c-Met-expressing tumor. (I) has  
 CC selectivity for c-Met that is at least 100 times greater than their  
 CC selectivity for insulin like growth factor I receptor. This sequence  
 CC corresponds to the amino acid sequence for a germline antibody light  
 CC chain used in the invention.

XX Sequence 128 AA;

Query Match 95.9%; Score 535; DB 9; Length 128;

Best Local Similarity 96.3%; Pred. No. 3e-33;

Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYATSSRATGIP 80

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPSCSFQGQTKLEIK 108

DB 81 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPYTFQGQTKLEIK 128

RESULT 11

ID AAR38672 standard; protein; 129 AA.

XX AAR38672;

XX 25-MAR-2003 (revised)

DT 01-NOV-1993 (first entry)

XX vk325-Jk2.

XX Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS; CD4;  
 KW receptor; hybridoma; polymerase chain reaction; PCR; heavy; light; chain;  
 KW epitope; immune deficiency.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..116

FT Peptide /label= vk325

FT /label= sig\_peptide

FT Misc-difference 1 /note= "Met encoded by ATC (sic)"

FT Protein 21..129

FT /label= mat\_protein

FT Misc-difference 35 /note= "Pro encoded by GCA (sic)"

FT Region 44..55

FT /label= CDR1

FT Region 71..77



multiple sclerosis; neuroprotective; neurological disease;  
myasthenia gravis; muscular-gen.; neuroprotective; Crohn's disease;  
antifungal; gastrointestinal-gen.; nephritis; nephrotropic;  
genitourinary disease; primary biliary cirrhosis; hepatotropic;  
pancreatitis; allergy; antiallergic; contact dermatitis; dermatological;  
delayed hypersensitivity; inflammatory bowel disease; septic shock;  
antibacterial; infection; osteoporosis; osteopathic; degeneration;  
endocrine disease; musculoskeletal disease; osteoarthritis;  
antiarthritic; osteopathic; musculoskeletal disease; cognitive disorder;  
neuropathic; hereditary hemorrhagic telangiectasia; vasotropic; restenosis;  
fungal infection; fungicide; parasitic infection; antiparasitic;  
viral infection; cytomegalovirus infection; virucide.  
Homo sapiens.  
WO2006055809-A2.  
26-MAY-2006.  
18-NOV-2005; 2005WO-US041904.  
18-NOV-2004; 2004US-0628815P.  
(IMCL-) IMCLONE SYSTEMS INC.  
Wu Y, Hicklin DJ, Bohlen P;  
WPI; 2006-373517/38.  
N-PSDB; AEH89260.

New isolated human monoclonal antibody that binds specifically to  
vascular endothelial growth factor receptor-1 for treating cancers and  
angiogenic-related disorders, e.g. atherosclerosis.

Claim 6; SEQ ID NO 15; 82pp; English.

The invention relates to an isolated human monoclonal antibody or  
fragment that binds specifically to vascular endothelial growth factor  
receptor-1 (VEGFR-1) and comprises a light chain complementarity  
determining region-2 (CDR2) of 7 amino acids (SEQ ID NO: 2; see AEH89240)  
and a light chain CDR3 of 9 amino acids (SEQ ID NO: 3; see AEH89241). Also  
included are: an isolated polynucleotide comprising a nucleotide sequence  
encoding the antibody or its fragment; an isolated polynucleotide  
comprising a nucleotide sequence selected from (AEH89259 to AEH89265),  
the nucleotide sequence encoding an antibody or its fragment that  
specifically binds to VEGFR-1; an expression vector comprising the  
polynucleotide sequence linked to an expression sequence; a recombinant  
host cell comprising the expression vector; a method of producing an  
antibody or its fragment; a method of modulating activity of VEGFR-1 in a  
mammal; a method of inhibiting angiogenesis in a mammal; and a method of  
reducing tumor growth in a mammal. The antibody is used to inhibit  
angiogenesis and reduce tumor growth in a mammal. The monoclonal  
antibodies, polynucleotides, and methods are useful for treating  
angiogenic-related disorders (e.g. atherosclerosis, rheumatoid arthritis,  
neovascular glaucoma, proliferative retinopathy including proliferative  
diabetic retinopathy, macular degeneration, hemangiomas, angiofibromas,  
psoriasis, retinopathy of prematurity (retrolental fibroplastic), corneal  
graft rejection, insulin-dependent diabetes mellitus, multiple sclerosis,  
myasthenia gravis, Crohn's disease, autoimmune nephritis, primary biliary  
cirrhosis, acute pancreatitis, allograft rejection, allergic inflammation  
(allergic reaction), contact dermatitis and delayed hypersensitivity  
reactions, inflammatory bowel disease, septic shock, osteoporosis,  
osteoarthritis, cognitive defects induced by neuronal inflammation, Osler  
-Weber syndrome (hereditary hemorrhagic telangiectasia), restenosis, and  
fungal, parasitic and viral infections, including cytomegaloviral  
infections). The present sequence represents anti-VEGFR-1 antibody light  
chain variable region SEQ ID NO:15.

Sequence 120 AA;

Query Match 95.5%; Score 533; DB 10; Length 120;  
Best Local Similarity 95.4%; Pred. No. 4e-33;  
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60  
DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60  
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYSGSSPCSGQGTGLEIK 108  
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYSGSSPLTFGGQGTGLEIK 108

# RESULT 14

ID ABJ36930 standard; protein; 130 AA.

AC ABJ36930;

DT 01-MAY-2003 (first entry)

DE Anti-CD40 monoclonal antibody related protein SEQ ID No 46.

KW Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;  
KW human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;  
KW dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;  
KW immunoadjuvant; anti-tumour agent; immunosuppressant; allergy;  
KW autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.

OS Unidentified.

XX WO200288186-A1.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-JP004292.

XX 27-APR-2001; 2001WO-US013672.

XX 11-MAY-2001; 2001JP-00142482.

XX 05-OCT-2001; 2001JP-00310535.

XX 26-OCT-2001; 2001US-00040244.

XX (KIRI ) KIRIN BEER KK.

XX Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;

XX WPI; 2003-120463/11.

XX N-PSDB; ABT31872.

XX Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,  
or functional fragment, is useful in the treatment of e.g. autoimmune  
diseases or cancer.

XX Claim 25; Page 51; 94pp; Japanese.

The invention relates to an antibody to human CD40, or its functional  
fragment, has at least one of the following properties: acting on  
dendritic cells to produce IL-12 in the presence of LPS  
(lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic  
cells to activate maturity of the dendritic cells with high G28-5  
antibody; and activating CD95 expression with high G28-5 antibody against  
B cell line. Such antibodies or functional fragments can be used as  
immunoadjuvants, anti-tumour agents, immunosuppressants, and as remedies  
for autoimmune diseases, allergy or coagulation factor VIII inhibitors  
syndrome. This sequence represents a protein relating to the anti-CD40  
monoclonal antibody of the invention

XX Sequence 130 AA;

Query Match 95.5%; Score 533; DB 6; Length 130;  
Best Local Similarity 95.4%; Pred. No. 4.3e-33;  
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60  
DB 21 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 80

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPCSFQGGTKLEIK 108  
 Db 81 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPITFGQGRLEIK 128

RESULT 15

AE995253  
 ID AEG95253 standard; protein; 130 AA.

XX AC AEG95253;

XX DT 01-JUN-2006 (first entry)

DE DE Human immunoglobulin G4 (IgG4) antibody related protein SEQ ID NO 8.  
 XX immunosuppressive; antiinflammatory; gastrointestinal-gen.; antitumor;  
 KW dermatological; hemostatic; neuroprotective; antipsoriatic;  
 KW antirheumatic; cytostatic; antiarteriosclerotic; nephrotropic;  
 KW immunostimulator; immunoglobulin; IgG4; transplant rejection;  
 KW immune disorder; systemic lupus erythematosus; dermatological disease;  
 KW metabolic disorder; musculoskeletal disease;  
 KW idiopathic thrombocytopenic purpura; genetic disorder;  
 KW hematological disease; neurological disease; multiple sclerosis;  
 KW psoriasis; dermatological disease; rheumatism; inflammation; cancer;  
 KW neoplasm; arteriosclerosis; cardiovascular disease; nephritis;  
 KW genitourinary disease; Alzheimers disease; degeneration; amyloidosis.

XX OS Homo sapiens.

XX WO2006033386-A1.

XX PD 30-MAR-2006.

XX PF 22-SEP-2005; 2005WO-JP017463.

XX PR 22-SEP-2004; 2004JP-00275908.

XX PA (KIRI ) KIRIN BEER KK.

XX PI Takahashi N, Yoshida H;

XX DR WPI; 2006-316320/33.

XX DR N-PSDB; AEG95252.

XX Novel anti-CD40 antibody having heavy chain constant region of human  
 PT immunoglobulin G4 including substitution of arginine at specific position  
 PT by lysine, threonine, methionine or leucine, useful in treating autoimmune  
 PT disease and cancer.

PS Example 1; SEQ ID NO 8; 47pp; Japanese.

XX The invention relates to an antibody comprising heavy chain constant  
 CC region of human immunoglobulin G4 (IgG4). The antibody being anti-CD40  
 CC antibody is useful as therapeutic agent of transplant rejection.  
 CC autoimmune disease, cancer, arteriosclerosis, nephritis, Alzheimer's  
 CC disease or amyloidosis. The antibody is useful for treating transplant  
 CC rejection, autoimmune disease (e.g. inflammatory bowel disease, Crohn's  
 CC disease and ulcerative colitis), systemic lupus erythematosus (SLE),  
 CC idiopathic thrombocytopenic purpura (ITP) multiple sclerosis, psoriasis,  
 CC rheumatism, cancer (e.g. lung cancer, colon cancer, rectal cancer, breast  
 CC pancreatic cancer, liver cancer, prostatic cancer, bladder cancer, cancer  
 CC and stomach cancer), arteriosclerosis, nephritis, Alzheimer's  
 CC disease and amyloidosis. The antibody exhibits suppressed aggregation  
 CC formation, and is highly stable mutant of IgG4 antibody. The antibody  
 CC exhibits decreased aggregate formation in low pH, and maintains binding  
 CC property with respect to the antigen, thus the side effects caused by  
 CC aggregate of the antibody can be avoided. The antibody has improved or  
 CC controlled antibody dependent cell-mediated cytotoxicity and/or  
 CC complement dependent cytotoxicity. The present sequence represents a  
 CC human immunoglobulin G4 (IgG4) antibody related protein. Note: The  
 CC sequence data for this patent was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ

Sequence 130 AA;

Query Match 95.5%; Score 533; DB 10; Length 130;  
 Best Local Similarity 95.4%; Pred. No. 4.3e-33;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOKPFGQAPRLLIYATSSRATGIP 60  
 Db 21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOKPFGQAPRLLIYATSSRATGIP 80  
 QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPCSFQGGTKLEIK 108  
 Db 81 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPITFGQGRLEIK 128

Search completed: April 25, 2007, 04:05:22  
 Job time : 94.661 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 8 Seconds  
(without alignments)  
1261.509 Million cell updates/sec

Title: US-10-665-383-4  
Perfect score: 558  
Sequence: 1 EIVLTQSPGTLSPGERAT.....COQYGSPPCSFGQGTKLEIK 108  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	535	95.9	108	2 C30608	Ig kappa chain V-I
2	535	95.9	109	2 H30601	Ig kappa chain V-I
3	534	95.7	109	2 H30601	Ig kappa chain V-I
4	533	95.5	109	2 H30601	Ig kappa chain V-I
5	531	95.2	109	2 PH0963	Ig kappa chain V-I
6	531	95.2	109	2 D30601	Ig kappa chain V-I
7	530	95.0	109	2 C30601	Ig kappa chain V-I
8	530	95.0	129	2 S46369	Ig kappa chain var
9	530	95.0	134	2 S38643	Ig kappa chain V-I
10	529	94.8	109	2 C30601	Ig kappa chain V-I
11	529	94.8	129	2 S49532	anti-Sm antibody V
12	528	94.6	129	1 K3HUA	Ig kappa chain pre
13	527	94.4	128	2 S20636	Ig kappa chain V-I
14	526	94.3	129	1 K3HUI	Ig kappa chain pre
15	524	93.9	109	1 K3HUI	Ig kappa chain V-I
16	524	93.9	109	2 F30607	Ig kappa chain V-I
17	523.5	93.8	114	2 S46375	Ig kappa chain V-I
18	521	93.4	109	1 K3HUI	Ig kappa chain V-I
19	520	93.2	109	2 A30608	Ig kappa chain V-I
20	515	92.3	109	2 C30607	Ig kappa chain V-I
21	514	92.1	107	2 PH0965	Ig kappa chain V-I
22	514	92.1	108	2 C30608	Ig kappa chain V-I
23	513	91.9	124	2 S20633	Ig kappa chain - h
24	511	91.6	121	2 S40327	Ig kappa chain - h
25	508	91.0	109	1 K3HUI	Ig kappa chain V-I
26	507	90.9	110	2 S20635	Ig kappa chain V-I
27	504.5	90.4	108	2 E30609	Ig kappa chain V-I
28	503.5	90.2	110	2 E30607	Ig kappa chain V-I
29	503	90.1	108	1 K3HUB6	Ig kappa chain V-I

30	502	90.0	109	2 F44151	Ig kappa chain V-I
31	501.5	89.9	108	2 F44151	Ig kappa chain V-I
32	500	89.6	109	1 K3HUGO	Ig kappa chain V-I
33	500	89.6	130	2 S20637	Ig kappa chain V-I
34	499	89.4	129	2 A32274	Ig kappa chain pre
35	497.5	89.2	110	2 S44120	Ig kappa chain V-I
36	495	88.7	109	2 S47181	Ig kappa chain - h
37	488.5	87.5	104	2 PH0964	Ig kappa chain V-I
38	488	87.5	215	2 JE0242	Ig kappa chain - h
39	486.5	87.2	129	2 S40325	Ig kappa chain V-I
40	485	86.9	96	2 A30601	Ig kappa chain V-I
41	484	86.9	116	2 B27594	Ig kappa chain pre
42	484	86.7	215	2 A23746	Ig kappa chain V-I
43	479	85.8	118	2 T03036	Ig light chain - h
44	477	85.5	108	2 S33988	Ig kappa chain V-I
45	475	85.1	116	2 C27594	Ig kappa chain pre

## ALIGNMENTS

## RESULT 1

C30608  
Ig kappa chain V-III region (Pie) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
C;Accession: C30608  
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon  
J. Immunol. 142, 3158-3163, 1989  
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies  
A;Reference number: A30601; MUID:89215279; PMID:2496160  
A;Accession: C30608  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-108 <GON>  
A;Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE3  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 535; DB 2; Length 108;  
Best Local Similarity 96.3%; Pred. No. 3.8e-38;  
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY	1	EIVLTQSPGTLSPGERATLSCRSQSVSSVLYATQKPGQAPRLLIYATSSRATGIP	60
DB	1	EIVLTQSPGTLSPGERATLSCRSQSVSSVLYATQKPGQAPRLLIYATSSRATGIP	60
QY	61	DRFSGSGSGTDFTLTISRLEPEDFAVYCOQYGSPPCSFGQGTKLEIK	108
DB	61	DRFSGSGSGTDFTLTISRLEPEDFAVYCOQYGSPPCSFGQGTKLEIK	108

## RESULT 2

H30601  
Ig kappa chain V-III region (Gar and Flo) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000  
C;Accession: H30601; E30601  
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon  
J. Immunol. 142, 3158-3163, 1989  
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies  
A;Reference number: A30601; MUID:89215279; PMID:2496160  
A;Accession: H30601  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-109 <GON>  
A;Cross-references: UNIPARC:UPI0000011B930  
A;Accession: E30601  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-109 <GON2>  
A;Cross-references: UNIPARC:UPI0000011B930



C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 535; DB 2; Length 109;  
Best Local Similarity 96.3%; Pred. No. 3.8e-38;  
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60  
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60  
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPCSFGQGTKEIK 108  
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPYTFGQGTKEIK 108

## RESULT 3

F30601  
Ig kappa chain V-III region (Neu) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000  
C:Accession: F30601  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soldo J. Immunol. 142, 3158-3163, 1989  
A:Title: Structural and idiotype characterization of the L chains of human IgM autoantibodies.  
A:Reference number: A30601; MUID:89215279; PMID:2496160  
A:Accession: F30601  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-109 <GON>  
A:Cross-references: UNIPARC:UPI0000176AE6  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 534; DB 2; Length 109;  
Best Local Similarity 93.5%; Pred. No. 4.6e-38;  
Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60  
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60  
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPCSFGQGTKEIK 108  
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPCTFGQGTKEIK 108

## RESULT 4

B30601  
Ig kappa chain V-III region (Glo) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: B30601  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soldo J. Immunol. 142, 3158-3163, 1989  
A:Title: Structural and idiotype characterization of the L chains of human IgM autoantibodies.  
A:Reference number: A30601; MUID:89215279; PMID:2496160  
A:Accession: B30601  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-109 <GON>  
A:Cross-references: UNIPARC:UPI0000176AE7  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.5%; Score 533; DB 2; Length 109;  
Best Local Similarity 95.4%; Pred. No. 5.6e-38;  
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60

DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60  
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPCSFGQGTKEIK 108  
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPYTFGQGTKEIK 108

## RESULT 5

PH0963  
Ig kappa chain V region (G6+ CLL-SMI) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C:Accession: PH0963  
R:Martin, T.; Duffy, S.P.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291  
A:Accession: PH0963  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-109 <MAR>  
A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176A29  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>  
F:16-91/Region: framework 1  
F:24-34/Region: complementarity-determining 1  
F:35-50/Region: framework 2  
F:51-56/Region: complementarity-determining 2  
F:57-89/Region: framework 3  
F:90-97/Region: complementarity-determining 3

Query Match 95.2%; Score 531; DB 2; Length 109;  
Best Local Similarity 95.4%; Pred. No. 8.2e-38;  
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60  
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60  
QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPCSFGQGTKEIK 108  
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCYQYGGSPYTFGQGTKEIK 108

## RESULT 6

D30601  
Ig kappa chain V-III region (Cur) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: D30601  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soldo J. Immunol. 142, 3158-3163, 1989  
A:Title: Structural and idiotype characterization of the L chains of human IgM autoantibodies.  
A:Reference number: A30601; MUID:89215279; PMID:2496160  
A:Accession: D30601  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-109 <GON>  
A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE9  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.2%; Score 531; DB 2; Length 109;  
Best Local Similarity 95.4%; Pred. No. 8.2e-38;  
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60  
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQQKPGQAPRLIIYATSSRATGIP 60



QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSPPCSFGQGTKEIK 108  
 |||||  
 Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSPPCSFGQGTKEIK 108  
 |||||

## RESULT 7

C30601  
 Ig kappa chain V-III region (Pay) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C:Accession: C30601  
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soló  
 J. Immunol. 142, 3158-3163, 1989  
 A:Title: Structural and idiotypic characterization of the L chains of human Igm autoanti  
 A:Reference number: A30601; MUID:89215279; PMID:2496160  
 A:Accession: C30601  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-109 <GON>  
 A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE6  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 109;  
 Best Local Similarity 94.4%; Pred. No. 9.9e-38;  
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIYATSSRATGIP 60  
 |||||  
 Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIYATSSRATGIP 60  
 |||||

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSPPCSFGQGTKEIK 108  
 |||||  
 Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSPPCSFGQGTKEIK 108  
 |||||

## RESULT 8

S46369  
 IG light chain variable region (VJ) - human  
 C:Species: Homo sapiens (man)  
 C>Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
 C:Accession: S46369  
 R;Bensimon, C.; Chastagner, P.; Zouali, M.  
 EMBO J. 13, 2951-2962, 1994  
 A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re  
 A:Reference number: S46369; MUID:94313975; PMID:8039491  
 A:Accession: S46369  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-129 <BEN>  
 A:Cross-references: UNIPARC:UPI0000176CA5; EMBL:Z27170  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 129;  
 Best Local Similarity 95.4%; Pred. No. 1.2e-37;  
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIYATSSRATGIP 60  
 |||||  
 Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIYATSSRATGIP 80  
 |||||

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSPPCSFGQGTKEIK 108  
 |||||  
 Db 81 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSPPCSFGQGTKEIK 128  
 |||||

## RESULT 9

S38643  
 IG kappa chain V region - human (fragment)  
 C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S38643  
 R;Bensimon, C.; Chastagner, P.; Zouali, M.  
 submitted to the EMBL Data Library, November 1993  
 A:Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.  
 A:Reference number: S38643  
 A:Accession: S38643  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-134 <BEN>  
 A:Cross-references: UNIPARC:UPI00001165A2; EMBL:Z27170; NID:9415955; PIDN:CRAA81694.1; PI  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F;41-116/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 134;  
 Best Local Similarity 95.4%; Pred. No. 1.2e-37;  
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIYATSSRATGIP 60  
 |||||  
 Db 26 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIYATSSRATGIP 85  
 |||||

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSPPCSFGQGTKEIK 108  
 |||||  
 Db 86 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSPPCSFGQGTKEIK 133  
 |||||

## RESULT 10

G30601  
 IG kappa chain V-III region (Got) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C:Accession: G30601  
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soló  
 J. Immunol. 142, 3158-3163, 1989  
 A:Title: Structural and idiotypic characterization of the L chains of human Igm autoanti  
 A:Reference number: A30601; MUID:89215279; PMID:2496160  
 A:Accession: G30601  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-109 <GON>  
 A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE6  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 529; DB 2; Length 109;  
 Best Local Similarity 95.4%; Pred. No. 1.2e-37;  
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIYATSSRATGIP 60  
 |||||  
 Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAYQKPGQAPRLIYATSSRATGIP 60  
 |||||

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSPPCSFGQGTKEIK 108  
 |||||  
 Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSPPCSFGQGTKEIK 108  
 |||||

## RESULT 11

S49532  
 anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human  
 C:Species: Homo sapiens (man)  
 C>Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 21-Jan-2000.  
 C:Accession: S49532  
 R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.  
 A:Reference number: S48797  
 A:Accession: S49532  
 A:Status: preliminary  
 A:Molecule type: mRNA

A;Accession: S20636  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-128 <LEE>  
A;Cross-references: UNIPARC:UPI00001163DC; EMBL:Z11894; NID:g33200; PIDN:CAA77948.1; PID:CAA77948.1; PID:CAA77948.1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 94.4%; Score 529; DB 2; Length 129;  
Best Local Similarity 95.4%; Pred. No. 1.4e-37;  
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60  
DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 80

QY 61 DRFSGSGGTDFLTITSLRLEPEDFAVYVCOQYGSSPCFQGTGLEIK 108  
DB 81 DRFSGSGGTDFLTITSLRLEPEDFAVYVCOQYGSSPCFQGTGLEIK 128

RESULT 12  
K3HUHA  
Ig kappa chain precursor V-III region (Hah) - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: P10022  
R;Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.  
J. Exp. Med. 167, 840-852, 1988  
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in chondrocytes  
A;Reference number: P10021; MUID:88171307; PMID:3127527  
A;Accession: P10022  
A;Molecule type: mRNA  
A;Residues: 1-129 <KIP>  
A;Cross-references: UNIPROT:P18135; UNIPARC:UPI000012E163  
A;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed in chondrocytes  
C;Genetics:  
A;Gene: GDB:IGKV3  
A;Cross-references: GDB:136266  
A;Map position: 2p12-2p11  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>  
F;21-117/Region: V segment  
F;36-111/Domain: immunoglobulin homology <IMM>  
F;44-55/Region: complementarity-determining 1  
F;71-77/Region: complementarity-determining 2  
F;110-117/Region: complementarity-determining 3  
F;118-129/Region: J segment (JK1)  
F;43-109/Disulfide bonds: #status predicted

Query Match 94.6%; Score 528; DB 1; Length 129;  
Best Local Similarity 94.4%; Pred. No. 1.7e-37;  
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60  
DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 80

QY 61 DRFSGSGGTDFLTITSLRLEPEDFAVYVCOQYGSSPCFQGTGLEIK 108  
DB 81 DRFSGSGGTDFLTITSLRLEPEDFAVYVCOQYGSSPCFQGTGLEIK 128

RESULT 13  
S20636  
Ig kappa chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S20636  
R;Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.  
submitted to the EMBL Data Library, April 1992  
A;Reference number: S20631

A;Accession: S20636  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-128 <LEE>  
A;Cross-references: UNIPARC:UPI00001163DC; EMBL:Z11894; NID:g33200; PIDN:CAA77948.1; PID:CAA77948.1; PID:CAA77948.1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 94.4%; Score 527; DB 2; Length 128;  
Best Local Similarity 94.4%; Pred. No. 2.1e-37;  
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60  
DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 80

QY 61 DRFSGSGGTDFLTITSLRLEPEDFAVYVCOQYGSSPCFQGTGLEIK 108  
DB 81 DRFSGSGGTDFLTITSLRLEPEDFAVYVCOQYGSSPCFQGTGLEIK 128

RESULT 14  
K3HUHI  
Ig kappa chain precursor V-III region (Hic) - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: P10021  
R;Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.  
J. Exp. Med. 167, 840-852, 1988  
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in chondrocytes  
A;Reference number: P10021; MUID:88171307; PMID:3127527  
A;Accession: P10021  
A;Molecule type: mRNA  
A;Residues: 1-129 <KIP>  
A;Cross-references: UNIPROT:P18136; UNIPARC:UPI000012E164  
A;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed in chondrocytes  
C;Genetics:  
A;Gene: GDB:IGKV3  
A;Cross-references: GDB:136266  
A;Map position: 2p12-2p11  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>  
F;21-117/Region: V segment  
F;36-111/Domain: immunoglobulin homology <IMM>  
F;44-55/Region: complementarity-determining 1  
F;71-77/Region: complementarity-determining 2  
F;110-117/Region: complementarity-determining 3  
F;118-129/Region: J segment (JK1)  
F;43-109/Disulfide bonds: #status predicted

Query Match 94.3%; Score 526; DB 1; Length 129;  
Best Local Similarity 94.4%; Pred. No. 2.5e-37;  
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60  
DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 80

QY 61 DRFSGSGGTDFLTITSLRLEPEDFAVYVCOQYGSSPCFQGTGLEIK 108  
DB 81 DRFSGSGGTDFLTITSLRLEPEDFAVYVCOQYGSSPCFQGTGLEIK 128

RESULT 15  
K3HUTI  
Ig kappa chain V-III region (Ti) - human  
C;Species: Homo sapiens (man)  
C;Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004

C;Accession: A01895  
 R;Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.  
 Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972  
 A;Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub  
 A;Reference number: A91651; MUID:72188439; PMID:5027703  
 A;Accession: A01895  
 A;Molecule type: protein  
 A;Residues: 1-109 <SUT>  
 A;Cross-references: UNIPROT:P01622; UNIPARC:UPI000012E15D  
 A;Note: the sequence of the C region, which has the Inv (3) marker, is also given  
 C;Comment: This is a Bence Jones protein.  
 C;Genetics:  
 A;Gene: GDB:IGKV3  
 A;Cross-references: GDB:136266  
 A;Map position: 2p12-2p11  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer  
 F;16-91/Domain: immunoglobulin homology <IMM>  
 F;23-89/Disulfide bonds: #status predicted

Query Match 33.9%; Score 524; DB 1; Length 109;  
 Best Local Similarity 92.6%; Pred. No. 3.2e-37;  
 Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY	1	EIVLTQSPGTLSPGERATLSCRAQSVSSVLA	WYQKPGQAPRLIIYATSSRATGIP	60
Db	1	EIVLTQSPGTLSPGERATLSCRAQSVNSFLA	WYQKPGQAPRLIIYVASSRATGIP	60
QY	61	DRFSGSGSGTDFTLTISRLEPEDFAVYQCQY	GGSPFCQGTKLEIK	108
Db	61	DRFSGSGSGTDFTLTISRLEPEDFAVYQCQY	GGSPFTFGQGTKVELK	108

Search completed: April 25, 2007, 04:06:40  
 Job time : 8.23729 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 74 Seconds  
(without alignments)  
1574.822 Million cell updates/sec

Title: US-10-665-383-4

Perfect score: 558

Sequence: 1 EIVLTQSPGTLISLSPERAT.....CQYGSPPCSFGQGTLEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 8.4.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528	94.6	129	1 KV3L HUMAN	P18135 homo sapien
2	526	94.3	129	1 KV3M HUMAN	P18136 homo sapien
3	524	93.9	109	1 KV3D HUMAN	P01622 homo sapien
4	521	93.4	109	1 KV3B HUMAN	P01620 homo sapien
5	518	92.8	109	2 Q9UL78 HUMAN	Q9UL78 homo sapien
6	508	91.0	109	1 KV3E HUMAN	P01623 homo sapien
7	506.5	90.8	236	2 Q6PI18 HUMAN	Q6PI18 homo sapien
8	504	90.3	109	2 Q9UL86 HUMAN	Q9UL86 homo sapien
9	503	90.1	108	1 KV3A HUMAN	P01619 homo sapien
10	500	89.6	109	1 KV3G HUMAN	P04206 homo sapien
11	493	88.4	235	2 Q6PJF2 HUMAN	Q6PJF2 homo sapien
12	491	88.0	235	2 Q6GMV9 HUMAN	Q6GMV9 homo sapien
13	481.5	86.3	236	2 Q6P5S8 HUMAN	Q6P5S8 homo sapien
14	466	83.5	100	1 KV3C HUMAN	P01621 homo sapien
15	465.5	83.4	128	1 KV3K HUMAN	P06311 homo sapien
16	446	79.9	109	1 KV3F HUMAN	P01624 homo sapien
17	445.5	79.8	234	2 Q5G9I9 HUMAN	Q5G9I9 homo sapien
18	439	78.7	129	1 KV3H HUMAN	P04207 homo sapien
19	435.5	78.0	108	2 Q9UL83 HUMAN	Q9UL83 homo sapien
20	426	76.3	109	2 Q9UL85 HUMAN	Q9UL85 homo sapien
21	420.5	75.4	115	1 KV3I HUMAN	P04433 homo sapien
22	420	75.3	235	2 Q6GMW0 HUMAN	Q6GMW0 homo sapien
23	415.5	74.5	114	1 KV4A HUMAN	P01625 homo sapien
24	414	74.2	116	1 KV3J HUMAN	P04434 homo sapien
25	399.5	71.6	134	1 KV4C HUMAN	P06314 homo sapien
26	398.5	71.4	108	2 Q9UL79 HUMAN	Q9UL79 homo sapien
27	397.5	71.2	108	1 KV1H HUMAN	P01600 homo sapien
28	394.5	70.7	236	2 Q6PIH7 HUMAN	Q6PIH7 homo sapien
29	390.5	70.0	108	2 Q9UL77 HUMAN	Q9UL77 homo sapien
30	387	69.4	133	1 KV4B HUMAN	P06313 homo sapien
31	386.5	69.3	108	2 Q9UL70 HUMAN	Q9UL70 homo sapien

32	386.5	69.3	236	2 Q6GMX8 HUMAN	Q6GMX8 homo sapien
33	384	68.8	114	2 Q8KIF1 MOUSE	Q8KIF1 mus musculus
34	383.5	68.7	131	2 Q81IC3 MOUSE	Q81IC3 mus musculus
35	382.5	68.5	108	1 KV1M HUMAN	P01605 homo sapien
36	382.5	68.5	236	2 Q6GMX9 HUMAN	Q6GMX9 homo sapien
37	382.5	68.5	236	2 Q7Z3Y4 HUMAN	Q7Z3Y4 homo sapien
38	381.5	68.4	244	2 Q6SZC8 HUMAN	Q6SZC8 homo sapien
39	381	68.3	107	2 Q96SA9 HUMAN	Q96SA9 homo sapien
40	380.5	68.2	108	1 KV1F HUMAN	P01598 homo sapien
41	379.5	68.0	108	1 KV1K HUMAN	P01603 homo sapien
42	378.5	67.8	234	2 Q7Z473 HUMAN	Q7Z473 homo sapien
43	377.5	67.7	236	2 Q6PIT5 HUMAN	Q6PIT5 homo sapien
44	377.5	67.7	240	2 Q6SZC9 HUMAN	Q6SZC9 homo sapien
45	376.5	67.5	255	2 Q6KB05 MOUSE	Q6KB05 mus musculus

#### ALIGNMENTS

RESULT 1  
KV3L\_HUMAN STANDARD; PRT; 129 AA.  
AC P18135;  
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.  
DT 01-NOV-1990, sequence version 1.  
DT 30-MAY-2006, entry version 43.  
DE Ig kappa chain V-III region HAH precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;  
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";  
RT J. Exp. Med. 167:840-852(1988).  
RL -I- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
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CC PIR; P18135; K3HUHA.  
CC HSSP; P01625; IEEO.  
CC SMR; P18135; 21-129.  
CC Ensembl; ENSG00000169769; Homo sapiens.  
CC LinkHub; P18135; -  
CC GO; GO:0005576; C:extracellular region; NAS.  
CC GO; GO:0003823; F:antigen binding; NAS.  
CC GO; GO:0006955; P:immune response; NAS.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003599; Ig\_sub.  
CC InterPro; IPR013106; Ig\_V-set.  
CC InterPro; IPR003596; Ig\_V-set\_sub.  
CC Pfam; PF07686; V-set; 1.  
CC SMART; SM00409; IG; 1.  
CC SMART; SM00406; IGV; 1.  
CC PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 129 Ig kappa chain V-III region HAH.  
FT REGION 21 43 /FTid=PRO\_0000015179.  
FT REGION 44 55 Framework-1.  
FT REGION 56 70 Complementarity-determining-1.  
FT REGION 71 77 Framework-2.  
FT REGION 78 109 Complementarity-determining-2.  
FT REGION 110 118 Framework-3.  
FT REGION 119 118 Complementarity-determining-3.

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FT REGION 119 129 JK1 segment.
FT DISULFID 43 109 By similarity.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 94.6%; Score 528; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 2.1e-47;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 80
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYVCOYGGSPCSFGQGTKEIK 108
Db 81 DRFGSGSGTDFLTISRLEPEDFAVYVCOYGGSPCSFGQGTKEIK 128

RESULT 2
KV3M HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 30-MAY-2006, entry version 43.
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC PIR; P18021; K3HUH1.
CC HSSP; P01625; 1EE0.
CC SMR; P18136; 21-129.
CC Ensembl; ENSG00000169769; Homo sapiens.
CC LinkHub; P18136; -.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig_sub.
CC InterPro; IPR013106; Ig_v-set.
CC Pfam; PF07686; V-set; 1.
CC SMART; SM00409; IG; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HIC.
FT FTId=PRO_0000015180.
FT
FT REGION 21 43 Framework-1.
FT REGION 44 55 Complementarity-determining-1.
FT REGION 56 70 Framework-2.
FT REGION 71 77 Complementarity-determining-2.
FT REGION 78 109 Framework-3.
FT REGION 110 118 Complementarity-determining-3.
FT REGION 119 129 JK1 segment.

FT REGION 119 129 JK1 segment.
FT DISULFID 43 109 By similarity.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 94.6%; Score 528; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 2.1e-47;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 80
QY 61 DRFGSGSGTDFLTISRLEPEDFAVYVCOYGGSPCSFGQGTKEIK 108
Db 81 DRFGSGSGTDFLTISRLEPEDFAVYVCOYGGSPCSFGQGTKEIK 128

RESULT 3
KV3D HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 30-MAY-2006, entry version 44.
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for the
RT mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC PIR; A01895; K3HUT1.
CC HSSP; P01625; 1LVE.
CC SMR; P01622; 1-109.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig_sub.
CC InterPro; IPR013106; Ig_v-set.
CC InterPro; IPR003596; Ig_v-set_sub.
CC Pfam; PF07686; V-set; 1.
CC SMART; SM00409; IG; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >109 Ig kappa chain V-III region Ti.
FT FTId=PRO_0000059764.
FT
FT DISULFID 23 89 By similarity.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 93.9%; Score 524; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 4.6e-47;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

```

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Db 1 EIVLTSPGTLSPGERATLSCRASQSVNSFLAWYQKPGQAPRLLIYVASSRATGIP 60
Qy 61 DRFGSGSGTDFLTISRLEPEDFAVYCOQYSSPCSGFGQTKLEIK 108
Db 61 DRFGSGSGTDFLTISRLEPEDFAVYCOQYSSPCSGFGQTKLEIK 108

RESULT 4
KV3B HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUN-1986, sequence version 1.
DE 30-MAY-2006, entry version 42.
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
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CC -----
DR PIR; A01892; KJHUS1.
DR HSSP; P01625; 1LVE.
DR SMR; P01620; 1-109.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig_v-set.
DR InterPro; IPR003596; Ig_v-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >109
FT DISULFID 23 89
FT NON TER 109 109
FT SEQUENCE 109 AA; 11775 MW; 76893ECD646FFB4 CRC64;
Query Match 93.4%; Score 521; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 9.6e-47;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTSPGTLSPGERATLSCRASQSVNSFLAWYQKPGQAPRLLIYATSSRATGIP 60
Db 1 EIVLTSPGTLSPGERATLSCRASQSVNSFLAWYQKPGQAPRLLIYATSSRATGIP 60
Qy 61 DRFGSGSGTDFLTISRLEPEDFAVYCOQYSSPCSGFGQTKLEIK 108
Db 61 DRFGSGSGTDFLTISRLEPEDFAVYCOQYSSPCSGFGQTKLEIK 108

RESULT 5
Q9UL78 HUMAN PRELIMINARY; PRT; 109 AA.
ID Q9UL78
AC Q9UL78;
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DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 18-APR-2006, entry version 23.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92228746; PubMed=1373487;
RA Zebedee S.L., Barbas C.F. 3rd, Hom Y.L., Caotien R.H., Graff R.,
RA DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;
RT "Human combinatorial antibody libraries to hepatitis B surface
RT antigen."
RL Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation."
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92202880; PubMed=1552291; DOI=10.1084/jem.175.4.983;
RA Martin T., Duffy S.F., Carson D.A., Kipps T.J.;
RT "Evidence for somatic selection of natural autoantibodies."
RL J. Exp. Med. 175:983-991(1992).
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CC -----
DR EMBL; AF035036; AAD56272.1; -; mRNA.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; H44151; H44151.
DR PIR; I30601; I30601.
DR PIR; PH0963; PH0963.
DR PIR; PH0964; PH0964.
DR PIR; PH0965; PH0965.
DR PIR; S33988; S33988.
DR PIR; S34096; S34096.
DR HSSP; P01625; 1EK3.
DR SMR; Q9UL78; 1-109.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig_v-set.
DR InterPro; IPR003596; Ig_v-set_sub.
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DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin domain.  
 FT NON\_TER 109 109  
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 92.8%; Score 518; DB 2; Length 109;  
 Best Local Similarity 93.5%; Pred. No. 2e-46;  
 Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSTLSPGERATLSCRAQSQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60  
 DB 1 EIVLTQSPGTLSTLSPGERATLSCRAQSQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60  
 QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCSFGQGTGLEIK 108  
 DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCSFGQGTGLEIK 108

RESULT 6  
 KV3E HUMAN STANDARD; PRT; 109 AA.  
 AC P01623;  
 RC TISSUE=Brain;  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=82046598; PubMed=6794615;  
 RA Andrews D.W., Capra J.D.;  
 RT "Amino acid sequence of the variable regions of light chains from two  
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa  
 RT group";  
 RL Biochemistry 20:5816-5822(1981).  
 CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma  
 CC globulin activity.  
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 CC -----  
 DR PIR; A01896; K3HVL.  
 DR HSP; P01625; LLVE.  
 DR SMR; P01623; 1-109.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; P:antigen binding; NAS.  
 DR GO; GO:0008955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003599; Ig\_sub.  
 DR InterPro; IPR013106; Ig\_V-set.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT CHAIN 1 >109 Ig kappa chain V-III region WOL.  
 FT DISULFID 23 89 /FTIDEPRO\_0000059765.  
 FT NON\_TER 109 109 By similarity.  
 SQ SEQUENCE 109 AA; 11746 MW; 566C115E69CBEE CRC64;

Query Match 91.0%; Score 508; DB 1; Length 109;  
 Best Local Similarity 91.7%; Pred. No. 2.2e-45;

Matches 99; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSTLSPGERATLSCRAQSQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60  
 DB 1 EIVLTQSPGTLSTLSPGERATLSCRAQSQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60  
 QY 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCSFGQGTGLEIK 108  
 DB 61 DRFSGSGGTDFLTISRLEPEDFAVYCCQYGGSPCSFGQGTGLEIK 108

RESULT 7  
 Q6PIL8 HUMAN PRELIMINARY; PRT; 236 AA.  
 ID O6PIL8\_HUMAN  
 AC O6PIL8  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 27-JUN-2006, entry version 20.  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
 CC histocompatibility complex class I molecules (By similarity).  
 CC -----  
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 CC -----  
 DR EMBL; BC032451; AAH32451.1; -; mRNA.  
 DR HSP; P01837; 1KCU.  
 DR SMR; Q6PIL8; 21-236.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR03597; Ig\_C1-set.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003599; Ig\_sub.  
 DR InterPro; IPR013106; Ig\_V-set.  
 DR InterPro; IPR003596; Ig\_V-set\_sub.



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DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IG1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
KW Transmembrane.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match          90.8%; Score 506.5; DB 2; Length 236;
Best Local Similarity 90.8%; Pred. No. 8.1e-45;
Matches 99; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 60
DB 21 ENVTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 80
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 108
DB 81 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 129

RESULT 8
Q9UL86 HUMAN PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
CC -----
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CC -----
DR EMBL; AF035028; RAD56264.1; -; mRNA.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSSP; P01625; 1EK3.
DR SMR; Q9UL86; 1-109.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 1
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72CDAC83 CRC64;

Query Match          90.3%; Score 504; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 5.9e-45;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 60
DB 21 ENVTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 80
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 108
DB 81 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 129

RESULT 9
KV3A HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 30-MAY-2006, entry version 40.
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP PROTEIN SEQUENCE.
RX PubMed=11946339; DOI=10.1016/0014-5793(69)80048-7;
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
RT of Bence Jones proteins Rad, Fr4 and B6.";
RL FEBS Lett. 2:301-304 (1969).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
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CC -----
DR PIR; A01891; K3HUB6.
DR HSSP; P01625; 1EEQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >108
FT -----
FT DISULFID 23 89
FT NON TER 108 108
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11636 MW; 8BC14FF07A419E3D CRC64;

Query Match          90.1%; Score 503; DB 1; Length 108;
Best Local Similarity 86.1%; Pred. No. 7.5e-45;
Matches 93; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 60
DB 21 ENVTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 80
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 108
DB 81 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 129

RESULT 10
KV3G HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987, integrated into UniProtKB/Swiss-Prot.
DT 20-MAR-1987, sequence version 1.
DT 30-MAY-2006, entry version 41.
DE Ig kappa chain V-III region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;  
 RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;  
 RT "Amino acid sequence of a light chain variable region of a human  
 RT rheumatoid factor of the Wa idiotype group, in part predicted by its  
 RT reactivity with antipeptide antibodies";  
 RL Mol. Immunol. 23:239-244 (1986).  
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 CC -----  
 CC PIR; A01893; K3HUGO.  
 DR HSP; P01625; 1EK3.  
 DR SMR; P04206; 1-109.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003599; Ig sub.  
 DR InterPro; IPR013106; Ig V-set.  
 DR InterPro; IPR003596; Ig\_V-set\_sub.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00409; IGV; 1.  
 DR PROSITE; PS0835; IG\_LIKE; 1.  
 DR Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT CHAIN 1 >109 Ig kappa chain V-III region GOL.  
 FT DISULFID 23 89 /FIDPRO\_0000059767.  
 FT NON TER 109 109 By similarity.  
 SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;  
 Query Match 89.6%; Score 500; DB 1; Length 109;  
 Best Local Similarity 89.8%; Pred. No. 1.6e-44;  
 Matches 97; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPGTLSPGERATLSCRASQSSVSSVLAWYQKPGQAPRLIYATSSRATGIP 60  
 DB 1 EIVLTQSPGTLSPGERATLSCRALSSRGVLAWYQKPGQAPRLIYATSSRATGIP 60  
 QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108  
 DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPRSPFGQGTKEIK 108  
 RESULT 11  
 Q6PJF2 HUMAN  
 ID Q6PJF2 HUMAN PRELIMINARY; PRT; 235 AA.  
 AC Q6PJF2  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 27-JUN-2006, entry version 21.  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
 RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Shvchenko Y.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; Smailus D.E.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
 CC histocompatibility complex class I molecules (By similarity).  
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 CC -----  
 CC EMBL; BC016380; AAH16380.1; -; mRNA.  
 DR HSP; P01837; 1KCU.  
 DR SMR; Q6PJF2; 21-235.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via ...; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig C1-set.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003599; Ig sub.  
 DR InterPro; IPR013106; Ig V-set.  
 DR InterPro; IPR003596; Ig\_V-set\_sub.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IGV; 1.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG\_LIKE; 2.  
 DR PROSITE; PS0290; IG\_MHC; UNKNOWN 1.  
 DR Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;  
 KW Transmembrane.  
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 Best Local Similarity 88.0%; Pred. No. 2.1e-43;  
 Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;  
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 DB 21 EIVLTQSPATLSLSPGERATLSCRAQIVSAVLAWYQKPGQAPRLIYATSSRATGIP 80  
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 DB 81 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSGTGGTGTVDIK 128  
 RESULT 12  
 Q6GMV9 HUMAN  
 ID Q6GMV9 HUMAN PRELIMINARY; PRT; 235 AA.  
 AC Q6GMV9  
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2004, sequence version 1.  
 DT 27-JUN-2006, entry version 21.  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
 CC histocompatibility complex class I molecules (By similarity).  
 CC -----  
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 CC -----  
 CC EMBL; BC073793; AAH73793.1; -; mRNA.  
 DR SMR; Q6GMV9; 21-235.  
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 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_C1-set.  
 DR InterPro; IPR003599; IG\_MHC.  
 DR InterPro; IPR013106; IG\_sub.  
 DR InterPro; IPR013106; IG\_V-set.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00407; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00407; IGV; 1.  
 DR PROSITE; PS00835; IG-LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;  
 KW Transmembrane.  
 SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;  
 Query Match 88.0%; Score 491; DB 2; Length 235;  
 Best Local Similarity 87.0%; Pred. No. 3.5e-43;  
 Matches 94; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 EIVLTSPGTLSPGERATLSCRSQSVSSVLAWYQKPGQAPRLIIYSSRATGIP 60  
 DQ |||||  
 Db 21 EIVLTSPGTLSPGERALSCRSQSVNSKYLAWYQKPGQAPRLIYASIRATGIP 80  
 QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCGQSSPSFGQGTLEIK 108  
 DQ |||||  
 Db 81 DRFGSGSGTDFTLTISRLESEDFALYFCQYGTSPITFGGKVEIK 128

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 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 27-JUN-2006, entry version 20.  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Glandular pool- thyroid;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
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 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Glandular pool- thyroid;  
 RX Strausberg R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
 CC histocompatibility complex class I molecules (By similarity).  
 CC -----  
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 CC -----  
 CC EMBL; BC062704; AAH62704.1; -; mRNA.  
 DR HSSP; P01837; 1KCU.  
 DR SMR; Q6P5S8; 21-236.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_C1-set.  
 DR InterPro; IPR003599; IG\_MHC.  
 DR InterPro; IPR013106; IG\_sub.  
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 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF07686; V-set; 1.  
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 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG-LIKE; 2.  
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 KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;  
 KW Transmembrane.

SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;  
 Query Match 86.3%; Score 481.5; DB 2; Length 236;  
 Best Local Similarity 85.3%; Pred. No. 3.5e-42;  
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 DT 30-MAY-2006, entry version 44.  
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 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Hominidae; Homo.  
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 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=84093600; PubMed=6419127; DOI=10.1038/307077a0;  
 RA Bentley D.L.;  
 RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to  
 RT a small family of germ-line V genes.";  
 RL Nature 307:77-80(1984).  
 CC -I- MISCELLANEOUS: This gene was isolated from the NG9/9.1 hybridoma.  
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 DR PIR; A01894; K3HUNG.  
 DR HSSP; P01625; 1EEQ.  
 DR SMR; P01621; 5-99.  
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 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003599; Ig sub.  
 DR InterPro; IPR013106; Ig\_V-set.  
 DR Pfam; PF07686; V-set; 1.  
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 DR Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.  
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DB 65 DRFSGSGSTDTLTISRLEPEDFAVYCCQYGNS 99  
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 DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JAN-1988, sequence version 1.  
 DT 30-MAY-2006, entry version 44.  
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 RX MEDLINE=86041852; PubMed=2997711;  
 RA Klobbeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;  
 RT "Human immunoglobulin kappa light chain genes of subgroups II and  
 RT III.";  
 RL Nucleic Acids Res. 13:6499-6513(1985).  
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 DR EMBL; Z00021; CAA77316.1; -; Genomic\_DNA.  
 DR PIR; A01899; K3HU41.  
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 DR SMR; P06311; 21-128.  
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 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003599; Ig sub.  
 DR InterPro; IPR013106; Ig\_V-set.  
 DR InterPro; IPR003596; Ig\_V-set\_sub.  
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 DR SMART; SM00409; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
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 FT REGION 21 43  
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 FT Complementarity-determining-2.  
 FT REGION 55 69  
 FT Complementarity-determining-3.  
 FT REGION 70 76  
 FT Complementarity-determining-3.  
 FT REGION 77 108  
 FT Complementarity-determining-3.  
 FT REGION 109 117  
 FT Complementarity-determining-3.  
 FT REGION 118 128  
 FT JKI segment.  
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 FT By similarity.  
 FT NON\_TER 128 128  
 SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;  
 Query Match 83.4%; Score 465.5; DB 1; Length 128;  
 Best Local Similarity 87.0%; Pred. No. 8.1e-41;  
 Matches 94; Conservative 4; Mismatches 9; Indels 1; Gaps 1;  
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 DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIYATSSRATGIP 79  
 QY 61 DRFSGSGSTDTLTISRLEPEDFAVYCCQYGSSP-CSFGQGTKEIK 108  
 DB 80 DRFSGSGSTDTLTISRLEPEDFAVYCCQYSTPYTGGTKEIK 127  
 Search completed: April 25, 2007, 04:06:37  
 Job time : 73.5254 secs

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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:06:51 ; Search time 14 Seconds  
(without alignments)  
696.311 Million cell updates/sec

Title: US-10-665-383-4

Perfect score: 558

Sequence: 1 EIVLTSPGTLSPGERAT.....CQYGSPPCSFGQTKLEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /EMC\_Celerra\_SID33/ptodata/2/iaa/5 COMB.pcp.\*
- 2: /EMC\_Celerra\_SID33/ptodata/2/iaa/6 COMB.pcp.\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/iaa/7 COMB.pcp.\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/iaa/8 COMB.pcp.\*
- 5: /EMC\_Celerra\_SID33/ptodata/2/iaa/9 COMB.pcp.\*
- 6: /EMC\_Celerra\_SID33/ptodata/2/iaa/RE COMB.pcp.\*
- 7: /EMC\_Celerra\_SID33/ptodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530	95.0	108	1	US-08-232-081B-42
2	529	94.8	109	2	US-09-025-769B-16
3	529	94.8	109	2	US-09-490-070A-16
4	529	94.8	109	2	US-09-490-153-16
5	529	94.8	109	2	US-09-490-324-16
6	528	94.6	108	2	US-09-644-668A-9
7	525	94.1	108	1	US-08-488-113B-150
8	525	94.1	108	1	US-08-477-484B-150
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10	525	94.1	108	2	US-08-839-765-150
11	525	94.1	108	2	US-09-136-389-150
12	525	94.1	108	2	US-09-610-838-150
13	525	94.1	108	2	US-09-711-485-150
14	524.5	94.0	226	2	US-09-456-090A-50
15	524.5	94.0	226	2	US-09-456-090A-86
16	524.5	94.0	226	2	US-09-453-234-50
17	524.5	94.0	226	2	US-09-453-234-86
18	522	93.5	108	2	US-09-644-668A-7
19	521	93.4	235	2	US-09-472-087-14
20	521	93.4	235	2	US-09-472-087-65
21	518.5	92.9	226	2	US-09-456-090A-80
22	518.5	92.9	226	2	US-09-453-234-80
23	518.5	92.9	236	2	US-09-859-053-34
24	518	92.8	108	2	US-09-240-274-178
25	518	92.8	108	2	US-09-848-798-178
26	513.5	92.0	236	2	US-09-859-053-38

27	512.5	91.8	226	2	US-09-456-090A-74	Sequence 74, Appl
28	512.5	91.8	226	2	US-09-453-234-74	Sequence 74, Appl
29	511.5	91.7	226	2	US-09-456-090A-42	Sequence 42, Appl
30	511.5	91.7	226	2	US-09-453-234-42	Sequence 42, Appl
31	511	91.6	129	1	US-08-480-774A-4	Sequence 4, Appl
32	508	91.0	108	1	US-07-634-278-86	Sequence 86, Appl
33	508	91.0	108	1	US-08-477-728-86	Sequence 86, Appl
34	508	91.0	108	1	US-08-474-040-86	Sequence 86, Appl
35	508	91.0	108	1	US-08-487-200-86	Sequence 86, Appl
36	508	91.0	108	1	US-08-484-537-86	Sequence 86, Appl
37	508	91.0	108	3	US-09-718-998-86	Sequence 86, Appl
38	506.5	90.8	226	2	US-03-456-090A-72	Sequence 72, Appl
39	506.5	90.8	226	2	US-09-453-234-72	Sequence 72, Appl
40	506	90.7	107	2	US-08-635-109-7	Sequence 7, Appl
41	506	90.7	107	2	US-08-844-215-10	Sequence 10, Appl
42	505	90.5	150	2	US-08-862-124-5	Sequence 5, Appl
43	505	90.5	287	2	US-08-862-124-17	Sequence 17, Appl
44	505	90.5	304	2	US-08-862-124-14	Sequence 14, Appl
45	504.5	90.4	107	1	US-08-107-669D-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-08-232-081B-42  
; Sequence 42, Application US/08232081B  
; Patent No. 5886152  
; GENERAL INFORMATION:  
; APPLICANT: NAKATANI, TOMOYUKI  
; APPLICANT: GOMI, HIDEYUKI  
; APPLICANT: WILDENES, JOHN  
; APPLICANT: NOGUCHI, HIROSHI  
; TITLE OF INVENTION: HUMANIZED B-B10  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,081B  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 20-3484  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-232-081B-42

Query Match 95.0%; Score 530; DB 1; Length 108;  
Best Local Similarity 94.4%; Pred. No. 1.6e-42;  
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCASQSVSSYLAWYQKPGQAPRIIYATSSBATGIP 60

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Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGSPCSFGQGTKEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGSPFLTFGQGTKEIK 108

RESULT 2
US-09-025-769B-16
; Sequence 16, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-16

Query Match 94.8%; Score 529; DB 2; Length 109;
Best Local Similarity 94.4%; Pred. No. 2e-42;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIP 60

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGSPCSFGQGTKEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGNSPYTFGQGTKEIK 108

RESULT 3
US-09-490-070A-16
; Sequence 16, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
```

```
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-070A-16

Query Match 94.8%; Score 529; DB 2; Length 109;
Best Local Similarity 94.4%; Pred. No. 2e-42;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIP 60

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGSPCSFGQGTKEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGNSPYTFGQGTKEIK 108

RESULT 4
US-09-490-153-16
; Sequence 16, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
```

STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-490-153-16

Query Match 94.8%; Score 529; DB 2; Length 109;  
Best Local Similarity 94.4%; Pred. No. 2e-42;  
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60  
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPCSFQGQTKLEIK 108  
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGNSPVTFGGQTKVEIK 108

RESULT 5  
US-09-490-324-16  
Sequence 16..Application US/09490324  
Patent No. 6828422  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-490-324-16

Query Match 94.8%; Score 529; DB 2; Length 109;  
Best Local Similarity 94.4%; Pred. No. 2e-42;  
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60  
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPCSFQGQTKLEIK 108  
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGNSPVTFGGQTKVEIK 108

RESULT 6  
US-09-644-668A-9  
Sequence 9, Application US/09644668A  
Patent No. 6984720  
GENERAL INFORMATION:  
APPLICANT: Koorman, Alan J.  
APPLICANT: Halk, Edward L.  
APPLICANT: Lonberg, Nils  
APPLICANT: Medarex, Inc.  
TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses  
FILE REFERENCE: 014643-010510US  
CURRENT APPLICATION NUMBER: US/09/644,668A  
FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/150,452  
PRIOR FILING DATE: 1999-08-24  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: light chain variable region predicted sequence for  
OTHER INFORMATION: 4B6 from V $\kappa$  A-27  
US-09-644-668A-9

Query Match 94.6%; Score 528; DB 2; Length 108;  
Best Local Similarity 94.4%; Pred. No. 2.5e-42;  
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60  
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPCSFQGQTKLEIK 108  
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGNSPVTFGGQTKVEIK 108

RESULT 7  
US-08-488-113B-150  
; Sequence 150, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Heid & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,113B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 150:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-488-113B-150

Query Match 94.1%; Score 525; DB 1; Length 108;  
Best Local Similarity 94.4%; Pred. No. 4.7e-42;  
Matches 102; Conservative 4; Indels 0; Gaps 0;  
QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSVYAWYQKPGQAPRLIIYATSSRATGIP 60  
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSVYAWYQKPGQAPRLIIYATSSRATGIP 60  
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYSSPCSGQGTKEIK 108  
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYSSPCSGQGTKEIK 108

RESULT 8  
US-08-477-484B-150  
; Sequence 150, Application US/08477484B  
; Patent No. 5756699  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Heid & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,484B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 150:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-477-484B-150

Query Match 94.1%; Score 525; DB 1; Length 108;  
Best Local Similarity 94.4%; Pred. No. 4.7e-42;  
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSVYAWYQKPGQAPRLIIYATSSRATGIP 60  
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSVYAWYQKPGQAPRLIIYATSSRATGIP 60  
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYSSPCSGQGTKEIK 108  
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYSSPCSGQGTKEIK 108



RESULT 9

US-08-646-360-150  
 ; Sequence 150, Application US/08646360  
 ; Patent No. 5837491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Better, Marc D.  
 ; APPLICANT: Carroll, Stephen F.  
 ; APPLICANT: Studnika, Gary M.  
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 ; TITLE OF INVENTION: Proteins  
 ; NUMBER OF SEQUENCES: 173  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 ; STREET: 500 West Madison Street, 34th floor  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60661  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/646,360  
 ; FILING DATE: 13-MAY-1996  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/05348  
 ; FILING DATE: 12-MAY-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/064,691  
 ; FILING DATE: 12-MAY-1993  
 ; APPLICATION DATA: US 07/988,430  
 ; FILING DATE: 09-DEC-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/901,707  
 ; FILING DATE: 19-JUN-1992  
 ; APPLICATION DATA: US 07/787,567  
 ; FILING DATE: 04-NOV-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McNicholas, Janet M.  
 ; REGISTRATION NUMBER: 32,918  
 ; REFERENCE/DOCKET NUMBER: 200-70.P4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312/707-8889  
 ; TELEFAX: 312/707-9155  
 ; TELEX: 650 388-1248  
 ; INFORMATION FOR SEQ ID NO: 150:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 108 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-646-360-150

Query Match 94.1%; Score 525; DB 1; Length 108;  
 Best Local Similarity 94.4%; Pred. No. 4.7e-42;  
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60  
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60  
 QY 61 DRPSGSGSGTDFLTISRLEPDPFAVYCCQYGSPPCSFGQGTKEIK 108  
 DB 61 DRPSGSGSGTDFLTISRLEPDPFAVYCCQYGSPPCSFGQGTKEIK 108

RESULT 10

US-08-839-765-150  
 ; Sequence 150, Application US/08839765  
 ; Patent No. 6146631  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Better, Marc D.  
 ; APPLICANT: Carroll, Stephen F.  
 ; APPLICANT: Studnika, Gary M.  
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 ; TITLE OF INVENTION: Proteins  
 ; NUMBER OF SEQUENCES: 169  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 ; STREET: 500 West Madison Street, 34th floor  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60661  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/839,765  
 ; FILING DATE: 15-APR-1997  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/425,336  
 ; FILING DATE: 18-APR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/064,691  
 ; FILING DATE: 12-MAY-1993  
 ; APPLICATION DATA: US 07/988,430  
 ; FILING DATE: 09-DEC-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/901,707  
 ; FILING DATE: 19-JUN-1992  
 ; APPLICATION DATA: US 07/787,567  
 ; FILING DATE: 04-NOV-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McNicholas, Janet M.  
 ; REGISTRATION NUMBER: 32,918  
 ; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312/707-8889  
 ; TELEFAX: 312/707-9155  
 ; TELEX: 650 388-1248  
 ; INFORMATION FOR SEQ ID NO: 150:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 108 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-839-765-150

Query Match 94.1%; Score 525; DB 2; Length 108;  
 Best Local Similarity 94.4%; Pred. No. 4.7e-42;  
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60  
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60  
 QY 61 DRPSGSGSGTDFLTISRLEPDPFAVYCCQYGSPPCSFGQGTKEIK 108  
 DB 61 DRPSGSGSGTDFLTISRLEPDPFAVYCCQYGSPPCSFGQGTKEIK 108

RESULT 11  
 US-09-136-389-150

Sequence 150, Application US/09136389  
Patent No. 6146850  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09136,389  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-136-389-150

Query Match 94.1%; Score 525; DB 2; Length 108;  
Best Local Similarity 94.4%; Pred. No. 4.7e-42;  
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60  
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60  
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYGGSSPCSPFGQGTKEIK 108  
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYGGSSPCSPFGQGTKEIK 108

RESULT 12

US-09-610-838-150  
Sequence 150, Application US/09610838  
Patent No. 6376217  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09610,838  
FILING DATE: 06-JUL-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09136,389  
FILING DATE: 18-AUG-1998  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-610-838-150

Query Match 94.1%; Score 525; DB 2; Length 108;  
Best Local Similarity 94.4%; Pred. No. 4.7e-42;  
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60  
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60  
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYGGSSPCSPFGQGTKEIK 108  
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYGGSSPCSPFGQGTKEIK 108

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RESULT 13
US-09-711-485-150
; Sequence 150, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroli, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,485
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/839,765
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70-P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-711-485-150

Query Match 94.1%; Score 525; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.7e-42;
Matches 102; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Qy 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSSPCSFQGTKEIK 108
Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSSPCSFQGTKEIK 108

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```

RESULT 14
US-09-456-090A-50
; Sequence 50, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456.090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 50
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-23L
US-09-456-090A-50

Query Match 94.0%; Score 524.5; DB 2; Length 226;
Best Local Similarity 95.4%; Pred. No. 1.2e-41;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Qy 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSS-PCSFQGTKEIK 108
Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSSPPYTFQGTKEIK 109

RESULT 15
US-09-456-090A-86
; Sequence 86, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456.090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 86
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-33L
US-09-456-090A-86

Query Match 94.0%; Score 524.5; DB 2; Length 226;
Best Local Similarity 95.4%; Pred. No. 1.2e-41;
Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
Qy 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSS-PCSFQGTKEIK 108
Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYVCOQYGSSPPYTFQGTKEIK 109

Search completed: April 25, 2007, 04:08:33
Job time : 14.5763 secs

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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 40 Seconds  
(without alignments)  
1251.741 Million cell updates/sec

Title: US-10-665-383-4  
Perfect score: 558  
Sequence: 1 EIVLTQSPGTLSPGERAT.....COQYSSPCSFQGTKEIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	108	4	US-10-041-860-49 Sequence 49, Appl
2	558	100.0	108	4	US-10-041-860-225 Sequence 225, App
3	558	100.0	108	4	US-10-041-860-259 Sequence 259, App
4	558	100.0	108	4	US-10-041-860-375 Sequence 375, App
5	558	100.0	108	4	US-10-665-383-4 Sequence 4, Appl
6	535	95.9	108	5	US-10-891-658-84 Sequence 84, Appl
7	535	95.9	108	5	US-10-891-658-131 Sequence 131, App
8	535	95.9	128	5	US-10-910-901-18 Sequence 18, Appl
9	533	95.5	108	4	US-10-309-762-156 Sequence 156, App
10	533	95.5	130	4	US-10-693-629-46 Sequence 46, Appl
11	532	95.3	108	4	US-10-737-724-123 Sequence 123, App
12	532	95.3	108	5	US-10-737-290-123 Sequence 123, App
13	532	95.3	109	5	US-10-725-962-27 Sequence 27, Appl
14	532	95.3	120	5	US-10-506-743-2 Sequence 2, Appl
15	532	95.3	130	5	US-10-737-290-161 Sequence 161, App
16	532	95.3	215	4	US-10-307-724-122 Sequence 122, App
17	532	95.3	215	5	US-10-737-290-122 Sequence 122, App
18	532	95.3	239	5	US-10-737-290-142 Sequence 142, App
19	530	95.0	384	4	US-10-291-265-804 Sequence 804, App
20	530	95.0	384	4	US-10-291-265-805 Sequence 805, App
21	530	95.0	384	4	US-10-291-265-806 Sequence 806, App
22	530	95.0	384	4	US-10-291-265-807 Sequence 807, App
23	530	95.0	384	6	US-11-000-463-804 Sequence 804, App
24	530	95.0	384	6	US-11-000-463-805 Sequence 805, App
25	530	95.0	384	6	US-11-000-463-806 Sequence 806, App
26	530	95.0	384	6	US-11-000-463-807 Sequence 807, App
27	529	94.8	108	4	US-10-269-711-21 Sequence 21, Appl

## ALIGNMENTS

### RESULT 1

US-10-041-860-49  
; Sequence 49, Application US/10041860  
; Publication No. US20030157109A1

GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadi

; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: ARGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041,860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49

; LENGTH: 108

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-041-860-49

Query Match 100.0%; Score 558; DB 4; Length 108;

Best Local Similarity 100.0%; Pred. No. 5e+0; Indels 0; Gaps 0;

Mismatches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSRASQSVSSSYLAWYQOKPGQAPRLLIYATSSRATGIP 60

DB 1 EIVLTQSPGTLSPGERATLSRASQSVSSSYLAWYQOKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFSGSGSGTFTLTISRLEPEDFVAVYCOQYSSPCSFQGTKEIK 108

DB 61 DRFSGSGSGTFTLTISRLEPEDFVAVYCOQYSSPCSFQGTKEIK 108

### RESULT 2

US-10-041-860-225

; Sequence 225, Application US/10041860

; Publication No. US20030157109A1

GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadi

28 529 94.8 108 4 US-10-684-109-21 Sequence 21, Appl

29 529 94.8 108 5 US-10-834-397-16 Sequence 16, Appl

30 528 94.6 108 3 US-09-948-939-9 Sequence 9, Appl

31 528 94.6 108 6 US-11-040-846-9 Sequence 9, Appl

32 528 94.6 247 6 US-11-056-825-8 Sequence 8, Appl

33 528 94.6 249 6 US-11-056-825-4 Sequence 4, Appl

34 526 94.3 108 4 US-10-338-366-4 Sequence 4, Appl

35 526 94.3 108 5 US-10-850-635-6 Sequence 6, Appl

36 526 94.3 109 4 US-10-371-942-112 Sequence 112, App

37 526 94.3 109 5 US-10-726-332-210 Sequence 210, App

38 526 94.3 109 5 US-10-938-353-114 Sequence 114, App

39 526 94.3 235 5 US-10-938-353-60 Sequence 60, Appl

40 525.5 94.2 131 4 US-10-478-056-27 Sequence 27, Appl

41 525.5 94.2 131 5 US-10-721-763-27 Sequence 27, Appl

42 525 94.1 106 4 US-10-309-762-163 Sequence 163, App

43 525 94.1 108 4 US-10-127-890-150 Sequence 150, App

44 525 94.1 108 5 US-10-717-243-150 Sequence 150, App

45 524.5 94.0 109 4 US-10-073-644C-8 Sequence 8, Appl

; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: ABGENIX.051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 225  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-225

Query Match 100.0%; Score 558; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 5e-40;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60  
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKLEIK 108  
Db 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKLEIK 108

## RESULT 3

US-10-041-860-259  
; Sequence 259, Application US/10041860  
; Publication No. US20030157109A1

; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gad

; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: ABGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041,860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 259

; LENGTH: 108

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-041-860-259

Query Match 100.0%; Score 558; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 5e-40;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60  
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKLEIK 108  
Db 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKLEIK 108

## RESULT 4

US-10-041-860-375

; Sequence 375, Application US/10041860

; Publication No. US20030157109A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gad  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: ABGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041,860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 375

; LENGTH: 108

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-041-860-375

Query Match 100.0%; Score 558; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 5e-40;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60  
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKLEIK 108  
Db 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKLEIK 108

## RESULT 5

US-10-665-383-4

; Sequence 4, Application US/10665383

; Publication No. US20040141969A1

; GENERAL INFORMATION:

; APPLICANT: Floege, Juergen

; APPLICANT: Gazit, Gad

; APPLICANT: Keyt, Bruce

; APPLICANT: LaRoche, William

; APPLICANT: Lichenstein, Henri

; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS

; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES

; FILE REFERENCE: ABGENIX.052A

; CURRENT APPLICATION NUMBER: US/10/665,383

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: 60/411,137

; PRIOR FILING DATE: 2002-09-16

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 108

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-665-383-4

Query Match 100.0%; Score 558; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 5e-40;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60  
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKLEIK 108  
Db 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKLEIK 108

## RESULT 6

US-10-891-658-84

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; Sequence 84, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-84

Query Match          95.9%; Score 535; DB 5; Length 108;
Best Local Similarity 96.3%; Pred. No. 4.5e-38;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPYTFGGQGTLEIK 108

RESULT 7
US-10-891-658-131
; Sequence 131, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 131
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-131

Query Match          95.9%; Score 535; DB 5; Length 108;
Best Local Similarity 96.3%; Pred. No. 4.5e-38;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPYTFGGQGTLEIK 108
```

```
Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPYTFGGQGTLEIK 108

RESULT 8
US-10-910-901-18
; Sequence 18, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO c-MET
; FILE REFERENCE: ABX-PP5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-18

Query Match          95.9%; Score 535; DB 5; Length 128;
Best Local Similarity 96.3%; Pred. No. 5.4e-38;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 21 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 80
QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108
DB 81 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPYTFGGQGTLEIK 128

RESULT 9
US-10-309-762-156
; Sequence 156, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-156

Query Match          95.5%; Score 533; DB 4; Length 108;
Best Local Similarity 95.4%; Pred. No. 6.7e-36;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108
DB 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPYTFGGQGTLEIK 108
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; OTHER INFORMATION: antibody light chain variable region
US-10-307-724-123

Query Match          95.3%; Score 532; DB 4; Length 108;
Best Local Similarity 95.4%; Pred. No. 8.2e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
   |||||
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGGSSPCSFQGTGKLEIK 108
   |||||
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGGSSPCSFQGTGKLEIK 108

RESULT 12
US-10-737-290-123
; Sequence 123, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Orenchia, Cecilia
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2 CIP III
; CURRENT APPLICATION NUMBER: US/10737,290
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/452,590
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/307,724
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 108
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain variable region
US-10-737-290-123

Query Match          95.3%; Score 532; DB 5; Length 108;
Best Local Similarity 95.4%; Pred. No. 8.2e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
   |||||
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGGSSPCSFQGTGKLEIK 108
   |||||
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGGSSPCSFQGTGKLEIK 108

RESULT 13
US-10-725-962-27
; Sequence 27, Application US/10725962
; Publication No. US20050013809A1
; GENERAL INFORMATION:
; APPLICANT: Samuel M. Owens
; APPLICANT: Frank I. Carroll
; APPLICANT: Philip Abraham
; APPLICANT: Melinda G. Gunnell

```

```

RESULT 10
US-10-693-629-46
; Sequence 46, Application US/10693629
; Publication No. US20040120948A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: MIKAYAMA, Toshifumi
; APPLICANT: YOSHIDA, Hitoshi
; APPLICANT: FORCE, Walker, R.
; APPLICANT: CHEN, Xingjie
; APPLICANT: TAKAHASHI, Nobuaki
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
; FILE REFERENCE: 021286-0306473
; CURRENT APPLICATION NUMBER: US/10/693,629
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP2001/142482
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: JP2001/310535
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US10/040,244
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-693-629-46

Query Match          95.5%; Score 533; DB 4; Length 130;
Best Local Similarity 95.4%; Pred. No. 8.1e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
   |||||
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 80

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGGSSPCSFQGTGKLEIK 108
   |||||
DB 81 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGGSSPCSFQGTGKLEIK 128

RESULT 11
US-10-307-724-123
; Sequence 123, Application US/10307724
; Publication No. US2003032972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2c1p
; CURRENT APPLICATION NUMBER: US/10/307,724
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 108
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:

```



```
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Xiao Feng
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; FILE REFERENCE: ABGENIX.071A
; CURRENT APPLICATION NUMBER: US/10/725,962
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430717
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-725-962-27

Query Match          95.3%; Score 532; DB 5; Length 109;
Best Local Similarity 95.4%; Pred. No. 8.3e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
   |||||
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPCSPGQGTKEIK 108
   |||||
Db 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPCSPGQGTKEIK 108
   |||||

RESULT 14
US-10-506-743-2
; Sequence 2, Application US/10506743
; Publication No. US20050106140A1
; GENERAL INFORMATION:
; APPLICANT: Lancaster, Joanne. Sloan
; TITLE OF INVENTION: Antagonistic Anti-hFas Ligand Human Antibodies and Fragments
; FILE REFERENCE: X15450 - National Stage
; CURRENT APPLICATION NUMBER: US/10/506,743
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/367,054
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-506-743-2

Query Match          95.3%; Score 532; DB 5; Length 120;
Best Local Similarity 95.4%; Pred. No. 9.1e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
   |||||
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPCSPGQGTKEIK 108
   |||||
Db 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPCSPGQGTKEIK 108
   |||||

RESULT 15
US-10-737-290-161
; Sequence 161, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Orcencia, Cecilia
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
```

```
; FILE REFERENCE: 1087-2 CIP III
; CURRENT APPLICATION NUMBER: US/10/737,290
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/452,590
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/307,724
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161
; LENGTH: 130
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: recombinant Ab Vk
US-10-737-290-161
```

```
Query Match          95.3%; Score 532; DB 5; Length 130;
Best Local Similarity 95.4%; Pred. No. 9.8e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
   |||||
Db 23 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 82
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPCSPGQGTKEIK 108
   |||||
Db 83 DRFSGSGGTDFLTISRLEPEDFAVYYCQYGSSPCSPGQGTKEIK 130
   |||||
```

Search completed: April 25, 2007, 04:22:51  
Job time : 39.9661 secs



```

; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-225

Query Match          100.0%; Score 558; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYQYGGSSPCSFQGTGLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYQYGGSSPCSFQGTGLEIK 108

RESULT 3
US-11-109-181-259
; Sequence 259, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-259

Query Match          100.0%; Score 558; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYQYGGSSPCSFQGTGLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYQYGGSSPCSFQGTGLEIK 108
```

```

RESULT 4
US-11-109-181-375
; Sequence 375, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-375

Query Match          100.0%; Score 558; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYQYGGSSPCSFQGTGLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYQYGGSSPCSFQGTGLEIK 108

RESULT 5
US-11-517-530-8
; Sequence 8, Application US/11517530
; Publication No. US20070065444A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Amgen Fremont Inc.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1
; FILE REFERENCE: ABX-PF9 PROV
; CURRENT APPLICATION NUMBER: US/11/517,530
; CURRENT FILING DATE: 2006-09-06
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Human
US-11-517-530-8

Query Match          96.4%; Score 538; DB 7; Length 108;
Best Local Similarity 96.3%; Pred. No. 3.5e-42;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYQYGGSSPCSFQGTGLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYQYGGSSPCSFQGTGLEIK 108
```

## RESULT 6

US-11-517-530-4  
; Sequence 4, Application US/11517530  
; Publication No. US20070065444A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Amgen Fremont Inc.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1  
; FILE REFERENCE: ABX-PF9 PROV  
; CURRENT APPLICATION NUMBER: US/11/517,530  
; CURRENT FILING DATE: 2006-09-06  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 4  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Human  
US-11-517-530-4

Query Match 96.4%; Score 538; DB 7; Length 215;  
Best Local Similarity 96.3%; Pred. No. 7e-42; Indels 0; Gaps 0;  
Matches 104; Conservative 2; Mismatches 2

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQKPGQAPRLLIYATSSRATGIP 60  
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQKPGQAPRLLIYATSSRATGIP 60  
Qy 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPCSFQGGTKLEIK 108  
Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPITFGQGTLEIK 108

## RESULT 7

US-11-433-924-180  
; Sequence 180, Application US/11433924  
; Publication No. US20060286112A1  
; GENERAL INFORMATION:  
; APPLICANT: Kellermann, Sird-Aimee  
; APPLICANT: Poord, Orit  
; APPLICANT: Belouski, Shelley Sims  
; APPLICANT: Green, Larry L.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO  
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND  
; FILE REFERENCE: ABGENIX.120A  
; CURRENT APPLICATION NUMBER: US/11/433,924  
; CURRENT FILING DATE: 2006-05-12  
; PRIOR APPLICATION NUMBER: US 60/681,846  
; PRIOR FILING DATE: 2005-05-16  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 180  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-433-924-180

Query Match 96.1%; Score 536; DB 7; Length 108;  
Best Local Similarity 95.4%; Pred. No. 5.4e-42; Indels 0; Gaps 0;  
Matches 103; Conservative 2; Mismatches 3

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQKPGQAPRLLIYATSSRATGIP 60  
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQKPGQAPRLLIYATSSRATGIP 60  
Qy 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPCSFQGGTKLEIK 108  
Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSAACSFQGGTKLEIK 108

## RESULT 8

US-11-517-530-132

US-11-517-530-132  
; Sequence 132, Application US/11517530  
; Publication No. US20070065444A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Amgen Fremont Inc.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1  
; FILE REFERENCE: ABX-PF9 PROV  
; CURRENT APPLICATION NUMBER: US/11/517,530  
; CURRENT FILING DATE: 2006-09-06  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 132  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Human  
US-11-517-530-132

Query Match 95.5%; Score 533; DB 7; Length 108;  
Best Local Similarity 95.4%; Pred. No. 1e-41; Indels 0; Gaps 0;  
Matches 103; Conservative 2; Mismatches 3

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQKPGQAPRLLIYATSSRATGIP 60  
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQKPGQAPRLLIYATSSRATGIP 60  
Qy 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPCSFQGGTKLEIK 108  
Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSSPITFGQGTLEIK 108

## RESULT 9

US-11-633-716-46  
; Sequence 46, Application US/11633716  
; Publication No. US20070077242A1  
; GENERAL INFORMATION:  
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
; APPLICANT: MIKAYAMA, Toshifumi  
; APPLICANT: YOSHIDA, Hitoshi  
; APPLICANT: FORCE, Walker, R.  
; APPLICANT: CHEN, Xingjie  
; APPLICANT: TAKAHASHI, Nobuaki  
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY  
; FILE REFERENCE: 021286-0358923  
; CURRENT APPLICATION NUMBER: US/11/633,716  
; CURRENT FILING DATE: 2006-12-05  
; PRIOR APPLICATION NUMBER: 10/693,629  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: PCT/US01/13672  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US09/844,684  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: JP2001/142482  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: JP2001/310535  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: US10/040,244  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-633-716-46

Query Match 95.5%; Score 533; DB 7; Length 130;  
Best Local Similarity 95.4%; Pred. No. 1.2e-41; Indels 0; Gaps 0;  
Matches 103; Conservative 2; Mismatches 3

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQKPGQAPRLLIYATSSRATGIP 60  
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWSYQKPGQAPRLLIYATSSRATGIP 80



Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSSPRTFGQGTKEIK 108

Search completed: April 25, 2007, 04:27:44  
Job time : 41.6441 secs

RESULT 14

US-11-009-410-22  
; Sequence 22, Application US/11009410  
; Publication No. US20070014724A1  
; GENERAL INFORMATION:  
; APPLICANT: Witte, Alison  
; APPLICANT: Williams, Denise  
; APPLICANT: Cardarelli, Josephine M.  
; APPLICANT: King, David  
; APPLICANT: Passmore, David  
; TITLE OF INVENTION: INTERFERON ALPHA ANTIBODIES AND THEIR USES  
; FILE REFERENCE: 04280/1200696-US1  
; CURRENT APPLICATION NUMBER: US/11/009,410  
; CURRENT FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: 60/528,757  
; PRIOR FILING DATE: 2003-12-10  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 22  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-009-410-22

Query Match 94.6%; Score 528; DB 7; Length 108;  
Best Local Similarity 94.4%; Pred. No. 2.9e-41;  
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSSPCSPFGQGTKEIK 108

Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSSPRTFGQGTKEIK 108

RESULT 15

US-11-009-410-24  
; Sequence 24, Application US/11009410  
; Publication No. US20070014724A1  
; GENERAL INFORMATION:  
; APPLICANT: Witte, Alison  
; APPLICANT: Williams, Denise  
; APPLICANT: Cardarelli, Josephine M.  
; APPLICANT: King, David  
; APPLICANT: Passmore, David  
; TITLE OF INVENTION: INTERFERON ALPHA ANTIBODIES AND THEIR USES  
; FILE REFERENCE: 04280/1200696-US1  
; CURRENT APPLICATION NUMBER: US/11/009,410  
; CURRENT FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: 60/528,757  
; PRIOR FILING DATE: 2003-12-10  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-009-410-24

Query Match 94.6%; Score 528; DB 7; Length 108;  
Best Local Similarity 94.4%; Pred. No. 2.9e-41;  
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSSPCSPFGQGTKEIK 108

Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSSPRTFGQGTKEIK 108

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 109 Seconds  
(without alignments)  
564.248 Million cell updates/sec

Title: US-10-665-383-22

Perfect score: 666

Sequence: 1 QVQLVQSGAEVKKPGASVKY.....VIVHYGMDVWGQGTTVTVSS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq 200701:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*  
11: Geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	666	100.0	126	7	ADK18597
2	666	100.0	126	7	ADK18870
3	666	100.0	126	7	ADK18812
4	666	100.0	126	7	ADK18775
5	666	100.0	126	8	ADL25412
6	605	90.8	126	7	ADK18925
7	605	90.8	126	7	ADK18780
8	605	90.8	126	7	ADK18616
9	605	90.8	126	7	ADK18817
10	605	90.8	126	8	ADL25448
11	604	90.7	126	7	ADK18864
12	604	90.7	126	7	ADK18595
13	604	90.7	126	7	ADK18777
14	604	90.7	126	8	ADL25408
15	600	90.1	126	7	ADK18778
16	600	90.1	126	7	ADK18613
17	600	90.1	126	7	ADK18815
18	600	90.1	126	8	ADL25464
19	593.5	89.1	125	7	ADK18614
20	593.5	89.1	125	7	ADK18779
21	593.5	89.1	125	7	ADK18919
22	593.5	89.1	125	7	ADK18816

23	593.5	89.1	125	8	ADL25444	AdL25444 Human mAb
24	593	89.0	122	6	ABR55829	ABR55829 Heavy cha
25	593	89.0	122	10	AEGL17553	Aeg17553 Human ang
26	591.5	88.8	127	10	AEJ20382	Aej20382 Anti-IRTA
27	590	88.6	125	7	ADK18814	AdK18814 Anti-huma
28	584.5	87.8	119	10	AEH94456	Aeh94456 Anti-ten-
29	584.5	87.8	123	10	AEK98538	Aek98538 Human ant
30	580.5	87.2	127	7	ADK18620	AdK18620 Anti-huma
31	580.5	87.2	127	7	ADK18818	AdK18818 Anti-huma
32	580.5	87.2	127	7	ADK18781	AdK18781 Anti-huma
33	580.5	87.2	127	7	ADK18936	AdK18936 Anti-huma
34	580.5	87.2	127	8	ADL25456	AdL25456 Human mAb
35	567.5	85.2	125	7	ADK18776	AdK18776 Anti-huma
36	567.5	85.2	125	7	ADK18948	AdK18948 Anti-huma
37	567.5	85.2	125	7	ADK18624	AdK18624 Anti-huma
38	567.5	85.2	125	7	ADK18813	AdK18813 Anti-huma
39	567.5	85.2	125	8	ADL25392	AdL25392 Human mAb
40	564.5	84.8	123	10	AEK98534	Aek98534 Human ant
41	564.5	84.8	476	2	AAW88464	Aaw88464 Monoclonal
42	559.5	84.0	123	9	AED87298	Aed87298 FV2A7 hea
43	557.5	83.7	109	10	AEH94503	Aeh94503 Human ger
44	554	83.2	450	10	AEK98141	Aek98141 Human 161
45	553.5	83.1	199	2	AAV34302	Aay34302 IgM antib

#### ALIGNMENTS

#### RESULT 1

ADK18597  
ID ADK18597 standard; protein; 126 AA.  
AC ADK18597;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Anti-human PDGF-D antibody heavy chain protein sequence.  
XX  
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057857-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 06-JAN-2003; 2003WO-US000398.  
XX  
PR 07-JAN-2002; 2002US-00041860.  
XX  
PA (ABGE-) ARGENIX INC.  
XX  
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
XX Bezabeh B;  
XX WPI; 2003-587119/55.  
XX  
XX New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.  
XX  
XX Disclosure; SEQ ID NO 21; 255pp; English.

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

Qy



Db 121 TTVSS 126

RESULT 4  
ADK18775  
ID ADK18775 standard; protein; 126 AA.

AC ADK18775;  
XX  
DT 06-MAY-2004 (first entry)

XX Anti-human PDGF-D antibody protein related sequence #1.  
DE  
XX  
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX Homo sapiens.

XX WO2003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.

XX Disclosure; SEQ ID NO 199; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.

XX Sequence 126 AA;

Query Match 100.0%; Score 666; DB 7; Length 126;  
Best Local Similarity 100.0%; Pred. No. 2.8e-53;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60  
DB 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60

QY 61 AQKFGQRTVMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120  
DB 61 AQKFGQRTVMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120

QY 121 TTVSS 126

DB 121 TTVSS 126

RESULT 5  
ADL25412  
ID ADL25412 standard; protein; 126 AA.

XX

AC ADL25412;

XX 17-JUN-2004 (first entry)

XX Human mAb 1.19 heavy chain variable region protein SEQ ID NO:22.

XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;  
KW nephritis; mesangial cell proliferation inhibition;  
KW mesangial proliferative glomerulonephritis; nephrotropic;  
KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;  
KW gene therapy; human; monoclonal antibody; mAb.

XX Homo sapiens.

XX WO2004024098-A2.

XX 25-MAR-2004.

XX 16-SEP-2003; 2003WO-US029414.

XX 16-SEP-2002; 2002US-0411137P.

XX (ABGE-) ABGENIX INC.

XX (CURA-) CURAGEN CORP.

XX Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;

XX WPI; 2004-269881/25.

XX N-PSDB; ADL25411.

XX Use of an antibody or its binding fragment that binds platelet derived  
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating  
PT nephritis.

XX Disclosure; SEQ ID NO 22; 115pp; English.

XX The present invention describes an antibody or its binding fragment that  
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is  
CC useful in preparing a medicament for treating nephritis. Also described:  
CC (1) a method of detecting nephritis; (2) a method of treating nephritis;  
CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method  
CC of treating mesangial proliferative glomerulonephritis. The antibody has  
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and  
CC antidiabetic activities, and can be used in gene therapy. The antibody or  
CC its binding fragment, that binds PDGF-DD, can be used in preparing a  
CC medicament for treating nephritis and related disorders, e.g., mesangial  
CC proliferative glomerulonephritis. The present sequence represents a human  
CC monoclonal antibody (mAb) variable region sequence, which is used in the  
CC exemplification of the present invention.

XX Sequence 126 AA;

Query Match 100.0%; Score 666; DB 8; Length 126;  
Best Local Similarity 100.0%; Pred. No. 2.8e-53;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60  
DB 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60

QY 61 AQKFGQRTVMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120  
DB 61 AQKFGQRTVMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120

QY 121 TTVSS 126

DB 121 TTVSS 126

RESULT 6  
ADK18925  
ID ADK18925 standard; protein; 126 AA.

XX

```
AC ADK18925;
XX
XX 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody protein related sequence #151.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 349; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 126 AA;
XX
XX Query Match 90.8%; Score 605; DB 7; Length 126;
XX Best Local Similarity 89.7%; Pred. No. 1.1e-47;
XX Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
XX
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGY 60
QY 61 AQKFGQRTVMTNTSISTAYMELSLRSEDYAVYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVMTNTSISTAYMELSLRSEDYAVYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126
XX
XX RESULT 8
XX ADK18616
XX ID ADK18616 standard; protein; 126 AA.
XX
XX AC ADK18616;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody heavy chain protein sequence.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX Anti-human PDGF-D antibody protein related sequence #6.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
```

```
ADK18780;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #151.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2003057857-A2.
XX
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 349; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 126 AA;
XX
XX Query Match 90.8%; Score 605; DB 7; Length 126;
XX Best Local Similarity 89.7%; Pred. No. 1.1e-47;
XX Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
XX
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGY 60
QY 61 AQKFGQRTVMTNTSISTAYMELSLRSEDYAVYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVMTNTSISTAYMELSLRSEDYAVYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126
XX
XX RESULT 7
XX ADK18780
XX ID ADK18780 standard; protein; 126 AA.
XX
XX AC ADK18780;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #6.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
```

PR 07-JAN-2002; 2002US-00041860.  
XX (ABGE-) ABGENIX INC.  
PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
XX Bezabeh B;  
PI WPI; 2003-587119/55.  
XX  
XX New human monoclonal antibody that binds to platelet-derived growth  
XX factor-D (PDGF-D), useful for treating chronic and recurrent human  
XX diseases, such as inflammation, autoimmunity and cancer.  
XX  
XX Disclosure; SEQ ID NO 40; 255pp; English.  
XX  
XX The invention relates to a human monoclonal antibody that binds to  
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
XX treating chronic and recurrent human diseases, such as inflammation,  
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
XX useful for modulating collagen formation, and for staging various  
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
XX generated using an active protein fragment of the gene product from the  
XX clone 30664188.0.99 arising in the conditioned medium obtained when  
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
XX sequence corresponds to a protein used in the invention.  
XX  
XX Sequence 126 AA;  
XX  
XX Query Match 90.8%; Score 605; DB 7; Length 126;  
XX Best Local Similarity 89.7%; Pred. No. 1.le-47;  
XX Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
XX  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60  
QY 61 AQKFGQRTVTMTNTSISTAYMELSSLSRSEDYAVYICARDVMITFGGVIVHYGMDVWGQGT 120  
DB 61 AQKFGQRTVTMTNTSISTAYMELSSLSRSEDYAVYICARDIVVVVVTATDYYTGMDVWGQGT 120  
QY 121 TTVTSS 126  
DB 121 TTVTSS 126  
RESULT 9  
ADK18817  
ID ADK18817 standard; protein; 126 AA.  
AC ADK18817;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Anti-human PDGF-D antibody protein related sequence #43.  
XX  
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX WO2003057857-A2.  
XX  
XX 17-JUL-2003.  
XX  
XX 06-JAN-2003; 2003WO-US000398.  
XX  
XX 07-JAN-2002; 2002US-00041860.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
XX Bezabeh B;  
XX WPI; 2003-587119/55.  
XX

XX New human monoclonal antibody that binds to platelet-derived growth  
XX factor-D (PDGF-D), useful for treating chronic and recurrent human  
XX diseases, such as inflammation, autoimmunity and cancer.  
XX  
XX Disclosure; SEQ ID NO 241; 255pp; English.  
XX  
XX The invention relates to a human monoclonal antibody that binds to  
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
XX treating chronic and recurrent human diseases, such as inflammation,  
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
XX useful for modulating collagen formation, and for staging various  
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
XX generated using an active protein fragment of the gene product from the  
XX clone 30664188.0.99 arising in the conditioned medium obtained when  
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
XX sequence corresponds to a protein used in the invention.  
XX  
XX Sequence 126 AA;  
XX  
XX Query Match 90.8%; Score 605; DB 7; Length 126;  
XX Best Local Similarity 89.7%; Pred. No. 1.le-47;  
XX Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
XX  
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60  
QY 61 AQKFGQRTVTMTNTSISTAYMELSSLSRSEDYAVYICARDVMITFGGVIVHYGMDVWGQGT 120  
DB 61 AQKFGQRTVTMTNTSISTAYMELSSLSRSEDYAVYICARDIVVVVVTATDYYTGMDVWGQGT 120  
QY 121 TTVTSS 126  
DB 121 TTVTSS 126  
RESULT 10  
ADL25448  
ID ADL25448 standard; protein; 126 AA.  
AC ADL25448;  
XX  
XX 17-JUN-2004 (first entry)  
XX  
XX Human mAb 1.46.1 heavy chain variable region protein SEQ ID NO:58.  
XX  
XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;  
XX nephritis; mesangial cell proliferation inhibition;  
XX mesangial proliferative glomerulonephritis; nephrotropic;  
XX antiinflammatory; dermatological; immunosuppressive; antidiabetic;  
XX gene therapy; human; monoclonal antibody; mAb.  
XX  
XX Homo sapiens.  
XX  
XX WO2004024098-A2.  
XX  
XX 25-MAR-2004.  
XX  
XX 16-SEP-2003; 2003WO-US029414.  
XX  
XX 16-SEP-2002; 2002US-0411137P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;  
XX WPI; 2004-269881/25.  
XX N-PSDB; ADL25447.  
XX  
XX Use of an antibody or its binding fragment that binds platelet derived  
XX growth factor-DD (PDGF-DD) for preparing a medicament for treating  
XX

PT nephritis.  
 PS Disclosure; SEQ ID NO 58; 115pp; English.  
 XX  
 CC The present invention describes an antibody or its binding fragment that  
 CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is  
 CC useful in preparing a medicament for treating nephritis. Also described:  
 CC (1) a method of detecting nephritis; (2) a method of treating nephritis;  
 CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method  
 CC of treating mesangial proliferative glomerulonephritis. The antibody has  
 CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and  
 CC antidiabetic activities, and can be used in gene therapy. The antibody or  
 CC its binding fragment, that binds PDGF-DD, can be used in preparing a  
 CC medicament for treating nephritis and related disorders, e.g., mesangial  
 CC proliferative glomerulonephritis. The present sequence represents a human  
 CC monoclonal antibody (mab) variable region sequence, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 126 AA;  
 Query Match 90.8%; Score 605; DB 8; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 1.1e-47;  
 Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60  
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60  
 QY 61 AQKFGRTVMTNTSISTAYMELSLRSEDYAVYICARDVMTFTGGVIVHYGMDVWGQGT 120  
 DB 61 AQKFGRTVMTNTSISTAYMELSLRSEDYAVYICARDVMTFTGGVIVHYGMDVWGQGT 120  
 QY 121 TTVTSS 126  
 DB 121 TTVTSS 126  
 RESULT 11  
 ADK18864  
 ID ADK18864 standard; protein; 126 AA.  
 XX  
 AC ADK18864;  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Anti-human PDGF-D antibody protein related sequence #90.  
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057857-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 06-JAN-2003; 2003WO-US000398.  
 XX  
 PR 07-JAN-2002; 2002US-00041860.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX  
 DR WPI; 2003-587119/55.  
 XX  
 CC New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 XX  
 PS Disclosure; SEQ ID NO 288; 255pp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody that binds to

CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
 CC sequence corresponds to a protein used in the invention.  
 XX  
 SQ Sequence 126 AA;  
 Query Match 90.7%; Score 604; DB 7; Length 126;  
 Best Local Similarity 91.3%; Pred. No. 1.4e-47;  
 Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60  
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60  
 QY 61 AQKFGRTVMTNTSISTAYMELSLRSEDYAVYICARDVMTFTGGVIVHYGMDVWGQGT 120  
 DB 61 AQKFGRTVMTNTSISTAYMELSLRSEDYAVYICAREGIAVAGTYTYYIGMDVWGQGT 120  
 QY 121 TTVTSS 126  
 DB 121 TTVTSS 126  
 RESULT 12  
 ADK18595  
 ID ADK18595 standard; protein; 126 AA.  
 XX  
 AC ADK18595;  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Anti-human PDGF-D antibody heavy chain protein sequence.  
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057857-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 06-JAN-2003; 2003WO-US000398.  
 XX  
 PR 07-JAN-2002; 2002US-00041860.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
 PI Bezabeh B;  
 XX  
 DR WPI; 2003-587119/55.  
 XX  
 CC New human monoclonal antibody that binds to platelet-derived growth  
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
 PT diseases, such as inflammation, autoimmunity and cancer.  
 XX  
 PS Disclosure; SEQ ID NO 19; 255pp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody that binds to  
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
 CC treating chronic and recurrent human diseases, such as inflammation,  
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
 CC useful for modulating collagen formation, and for staging various  
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
 CC generated using an active protein fragment of the gene product from the  
 CC clone 30664188.0.99 arising in the conditioned medium obtained when  
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This

CC sequence corresponds to a protein used in the invention.

XX Sequence 126 AA;

Query Match 90.7%; Score 604; DB 7; Length 126;  
Best Local Similarity 91.3%; Pred. No. 1.4e-47;  
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60

DB 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60

QY 61 AOKFQGRVTWTRNTSISTAYMELSSLSRSEDTAVYVCARDVMITFGGVIVHYGMDVWGQGT 120

DB 61 AOKFQGRVTWTRNTSISTAYMELSSLSRSEDTAVYVCAREGIAVAGTYYYYYGGMDVWGQGT 120

QY 121 TTVTVSS 126

DB 121 TTVTVSS 126

RESULT 13

ADK18777 ID ADK18777 standard; protein; 126 AA.

XX AC ADK18777;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-human PDGF-D antibody protein related sequence #3.

XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX OS Homo sapiens.

XX PN WO2003057857-A2.

XX PD 17-JUL-2003.

XX PF 06-JAN-2003; 2003WO-US000398.

XX PR 07-JAN-2002; 2002US-00041860.

XX PA (ABGE-) ABGENIX INC.

XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;

XX PI Bezabeh B;

XX DR WPI; 2003-587119/55.

XX PT New human monoclonal antibody that binds to platelet-derived growth

XX PT factor-D (PDGF-D), useful for treating chronic and recurrent human

XX PT diseases, such as inflammation, autoimmunity and cancer.

XX PS Disclosure; SEQ ID NO 201; 255pp; English.

XX CC The invention relates to a human monoclonal antibody that binds to

XX CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for

XX CC treating chronic and recurrent human diseases, such as inflammation,

XX CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are

XX CC useful for modulating collagen formation, and for staging various

XX CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were

XX CC generated using an active protein fragment of the gene product from the

XX CC clone 30664188.0.99 arising in the conditioned medium obtained when

XX CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This

XX CC sequence corresponds to a protein used in the invention.

XX SQ Sequence 126 AA;

Query Match

Best Local Similarity 90.7%; Score 604; DB 7; Length 126;

Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60

DB 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60

QY 61 AOKFQGRVTWTRNTSISTAYMELSSLSRSEDTAVYVCARDVMITFGGVIVHYGMDVWGQGT 120

DB 61 AOKFQGRVTWTRNTSISTAYMELSSLSRSEDTAVYVCAREGIAVAGTYYYYYGGMDVWGQGT 120

QY 121 TTVTVSS 126

DB 121 TTVTVSS 126

RESULT 14

ADL25408 ID ADL25408 standard; protein; 126 AA.

XX AC ADL25408;

XX DT 17-JUN-2004 (first entry)

XX DE Human mAb 1.18 heavy chain variable region protein SEQ ID NO:18.

XX KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;

XX KW nephritis; mesangial cell proliferation inhibition;

XX KW mesangial proliferative glomerulonephritis; nephrotropic;

XX KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;

XX KW gene therapy; human; monoclonal antibody; mAb.

XX OS Homo sapiens.

XX PN WO2004024098-A2.

XX PD 25-MAR-2004.

XX PF 16-SEP-2003; 2003WO-US029414.

XX PR 16-SEP-2002; 2002US-0411137P.

XX PA (ABGE-) ABGENIX INC.

XX PA (CURA-) CURAGEN CORP.

XX PI Floege J, Gazit-Bornstein G, Keyt B, Larochelle WJ, Lichenstein H;

XX PI WPI; 2004-269881/25.

XX DR N-PSDB; ADL25407.

XX PT Use of an antibody or its binding fragment that binds platelet derived

XX PT growth factor-DD (PDGF-DD) for preparing a medicament for treating

XX PT nephritis.

XX PS Disclosure; SEQ ID NO 18; 115pp; English.

XX CC The present invention describes an antibody or its binding fragment that

XX CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is

XX CC useful in preparing a medicament for treating nephritis. Also described:

XX CC (1) a method of detecting nephritis; (2) a method of treating nephritis;

XX CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method

XX CC of treating mesangial proliferative glomerulonephritis. The antibody has

XX CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and

XX CC antidiabetic activities, and can be used in gene therapy. The antibody or

XX CC its binding fragment, that binds PDGF-DD, can be used in preparing a

XX CC medicament for treating nephritis and related disorders, e.g., mesangial

XX CC proliferative glomerulonephritis. The present sequence represents a human

XX CC monoclonal antibody (mAb) variable region sequence, which is used in the

XX CC exemplification of the present invention.

XX SQ Sequence 126 AA;

Query Match

Best Local Similarity 90.7%; Score 604; DB 8; Length 126;

Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATCGGLEWMGMWNPNSGNTGY 60  
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATCGGLEWMGMWNPNSGNTGY 60  
QY 61 AQKFGQGRVTMTNTSISTAYMELSLRSEDYAVYICARDVMITFGGVIHYGMDVWGQGT 120  
Db 61 AQKFGQGRVTMTNTSISTAYMELSLRSEDYAVYICARDVMITFGGVIHYGMDVWGQGT 120  
QY 121 TTVTSS 126  
Db 121 TTVTSS 126

RESULT 15  
ADK18778  
ID ADK18778 standard; protein; 126 AA.  
AC ADK18778;  
XX 06-MAY-2004 (first entry)  
XX Anti-human PDGF-D antibody protein related sequence #4.  
DE antiinflammatory; immunomodulator; cytostatic; gene therapy.  
KW Homo sapiens.  
OS WO2003057857-A2.  
XX 17-JUL-2003.  
XX 06-JAN-2003; 2003WO-US000398.  
XX 07-JAN-2002; 2002US-00041860.  
XX (ABGE-) ABGENIX INC.  
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX WPI; 2003-587119/55.  
XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX Disclosure; SEQ ID NO 202; 255pp; English.  
XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
SQ Sequence 126 AA;

Query Match 90.1%; Score 600; DB 7; Length 126;  
Best Local Similarity 88.9%; Pred. No. 3.2e-47;  
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATCGGLEWMGMWNPNSGNTGY 60  
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATCGGLEWMGMWNPNSGNTGY 60  
QY 61 AQKFGQGRVTMTNTSISTAYMELSLRSEDYAVYICARDVMITFGGVIHYGMDVWGQGT 120  
Db 61 AQKFGQGRVTMTNTSISTAYMELSLRSEDYAVYICARDVMITFGGVIHYGMDVWGQGT 120

QY 121 TTVTSS 126  
Db 121 TTVTSS 126  
Search completed: April 25, 2007, 04:05:21  
Job time : 109.271 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 10 Seconds  
(without alignments)  
1261.509 Million cell updates/sec

Title: US-10-665-383-22

Perfect score: 666

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....VIVHYGMDVWGQGTIVTVSS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	569.5	85.5	127	2 S34014	Ig heavy chain V r
2	555	83.3	136	2 S31600	Ig heavy chain V r
3	530	79.6	132	2 S31596	Ig heavy chain V r
4	519.5	78.0	129	2 S46393	Ig heavy chain V r
5	517	77.6	98	2 S26918	Ig heavy chain V r
6	513	77.0	110	2 PH1670	Ig heavy chain V r
7	512	76.9	118	2 S36255	Ig heavy chain V r
8	504.5	75.8	142	2 A32483	Ig heavy chain V r
9	502	75.4	135	2 S49530	anti-Sm antibody V
10	495.5	74.4	123	2 D33548	Ig heavy chain V-1
11	493.5	74.1	129	2 S36260	Ig heavy chain V r
12	492	73.9	171	2 S23623	Ig heavy chain V r
13	486	73.0	118	2 PH1666	Ig heavy chain V r
14	486	73.0	124	2 S19665	Ig heavy chain V r
15	475.5	71.4	119	2 PH0961	Ig heavy chain V r
16	473.5	71.1	131	2 S26792	Ig heavy chain V r
17	467.5	70.2	127	2 PH0955	Ig heavy chain V r
18	466.5	70.0	122	2 S36271	Ig heavy chain V r
19	466	70.0	132	2 PH0934	Ig heavy chain V r
20	466	70.0	136	2 PH0960	Ig heavy chain V r
21	465	69.8	126	2 B33548	Ig heavy chain V-1
22	462.5	69.4	133	2 C33548	Ig heavy chain V-1
23	462.5	69.4	627	2 S14683	Ig mu chain precu
24	461	69.2	98	2 S26938	Ig heavy chain V r
25	461	69.2	114	2 PH1667	Ig heavy chain V r
26	461	69.2	117	2 S31680	Ig heavy chain V r
27	461	69.2	117	2 S18551	Ig heavy chain V r
28	461	69.2	122	2 PH0958	Ig heavy chain V r
29	460	69.1	120	2 S31999	Ig heavy chain V r

30	459.5	69.0	126	2 I44151	Ig heavy chain V r
31	457.5	68.7	160	2 PL0105	anti-PR2 erythrocy
32	456	68.5	110	2 PH1669	Ig heavy chain V r
33	453.5	68.1	109	2 PH1668	Ig heavy chain V r
34	453	68.0	98	2 S26912	Ig heavy chain V r
35	451.5	67.8	104	2 S69899	Ig heavy chain V r
36	451.5	67.8	121	2 S20783	Ig heavy chain V r
37	451.5	67.8	125	2 S68170	Ig heavy chain V r
38	451	67.7	143	1 ELHUND	Ig heavy chain pre
39	449.5	67.5	125	2 PH0957	Ig heavy chain V r
40	449.5	67.5	129	2 A33548	Ig heavy chain V-1
41	449	67.4	120	2 PH0962	Ig heavy chain V r
42	448.5	67.3	142	2 S19245	Ig heavy chain pre
43	446	67.0	120	2 S26789	Ig heavy chain V r
44	442	66.4	98	2 S26920	Ig heavy chain V r
45	442	66.4	128	2 PH0952	Ig heavy chain V r

#### ALIGNMENTS

##### RESULT 1

S34014

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996

C:Accession: S34014; S30535

R:Mariette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A>Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; MUID:93209281; PMID:7681398

A:Accession: S34014

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-127 <MAR>

A:Cross-references: UNIPARC:UPI0000176D31; EMBL:Z18321

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 569.5; DB 2; Length 127;  
Best Local Similarity 85.4%; Pred. No. 3.8e-44;  
Matches 111; Conservative 8; Mismatches 4; Indels 7; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKASGYFTSDYINVRQATGQGLEWMGNPNSGNTGY 60

Db 1 QVQMVQSGAEVKKPGASVKASGYFTSDYINVRQATGQGLEWMGNPNSGNTGY 60

QY 61 AQKFGQRTMTNTSISTAYMELSLRSRSDTAVYVCARDVMTFGGVIV---HYGMDVW 116

Db 61 AQKFGQRTMTNTSISTAYMELSLRSRSDTAVYFCARALSI---GVAIVIRGYVYALDVW 117

QY 117 GQGTIVTVSS 126

Db 118 GQGTIVSVSS 127

##### RESULT 2

S31600

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31600

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31595

A:Accession: S31600

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-136 <CUI>

A:Cross-references: UNIPARC:UPI0000116453; EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PII

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 555; DB 2; Length 136;  
Best Local Similarity 85.7%; Pred. No. 8.1e-43;  
Matches 108; Conservative 2; Mismatches 6; Indels 10; Gaps 1;  
  
Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60  
Db 20 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 79  
Qy 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDATVYICARDVMTFPGGVIVHYGMDVWGQGT 120  
Db 80 AQKFGQGVTVTRNTSISTAYMELSSLRSEDATVYICAR-----WRDAFDWGQGT 129  
Qy 121 TVTVSS 126  
Db 130 MVTVSS 135

RESULT 3  
S31596  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31596  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31596  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-132 <CUI>  
A;Cross-references: UNIPARC:UPI0000116454; EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 530; DB 2; Length 132;  
Best Local Similarity 82.5%; Pred. No. 1.4e-40;  
Matches 104; Conservative 3; Mismatches 5; Indels 14; Gaps 1;  
  
Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60  
Db 20 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDIDWVRQATGQGLEWMGWNPNNSGNTGY 79  
Qy 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDATVYICARDVMTFPGGVIVHYGMDVWGQGT 120  
Db 80 AQKFGQGVTVTRNTSISTAYMELSSLRSEDATVYILAK-----APAWGQGT 125  
Qy 121 TVTVSS 126  
Db 126 MVTVSS 131

RESULT 4  
S46393  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C;Accession: S46393  
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A;Reference number: S46390; MUID:94254092; PMID:8196048  
A;Accession: S46393  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-129 <FIG>  
A;Cross-references: UNIPARC:UPI000011663A; EMBL:Z31680; NID:G509786; PIDN:CAA83485.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 519.5; DB 2; Length 129;  
Best Local Similarity 79.1%; Pred. No. 1.2e-39;  
Matches 102; Conservative 8; Mismatches 16; Indels 3; Gaps 1;  
  
Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQGLEWMGWINPNSSGNTY 60  
Qy 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDATVYICARDVMTF---GGVIVHYGMDVWG 117  
Db 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDATVYICARDSAYYYDSSGGYSANYTMDVWG 120  
Qy 118 QGTTVTVSS 126  
Db 121 KGTTVTVSS 129

RESULT 5  
S26918  
Ig heavy chain V region (DP-15) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S26918  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
A;Reference number: S26885; MUID:93021117; PMID:1404388  
A;Accession: S26918  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-98 <TOM>  
A;Cross-references: UNIPARC:UPI0000031P36; EMBL:Z12317; NID:G32857; PIDN:CAA78187.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 517; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60  
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60  
Qy 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDATVYICAR 98  
Db 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDATVYICAR 98

RESULT 6  
PH1670  
Ig heavy chain V region (clone 2A12) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C;Accession: PH1670  
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo  
A;Reference number: PH1642; MUID:93301610; PMID:8315388  
A;Accession: PH1670  
A;Molecule type: mRNA  
A;Residues: 1-110 <HIL>  
A;Cross-references: UNIPARC:UPI00000176BEB  
A;Experimental source: B cell  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 513; DB 2; Length 110;  
Best Local Similarity 85.6%; Pred. No. 3.8e-39;  
Matches 101; Conservative 3; Mismatches 6; Indels 8; Gaps 2;



Qy 9 AEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGYAQKQGRV 68  
 Db 1 AEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGYAQKQGRV 60

Qy 69 TMTNTSISTAYMELSLRSEDYAVVYCARDVMTFGGVIVHYGMDVWGQTTVTVSS 126  
 Db 61 TMTNTSISTAYMELSLRSEDYAVVYCAR-----GKGGEF--DIWGQTLTVSS 110

RESULT 7  
 S36265  
 Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
 C:Accession: S36265  
 R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
 EMBO J. 12, 725-734, 1993  
 A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A:Reference number: S36256; MUID:93178448; PMID:7679990  
 A:Accession: S36265  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-118 <GRI>  
 A:Cross-references: UNIPARC:UPI0000118DE8; EMBL:Z18846; NID:G33121; PIDN:CAA79298.1; PID  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 512; DB 2; Length 118;  
 Best Local Similarity 78.6%; Pred. No. 5e-39;  
 Matches 99; Conservative 8; Mismatches 11; Indels 8; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60  
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60

Qy 61 AQKQGRVTMTNTSISTAYMELSLRSEDYAVVYCARDVMTFGGVIVHYGMDVWGQGT 120  
 Db 61 AQKQGRVTITRDTSASTAYMELSLRSEDYAVVYCARDFLSGY-----LDYWGQGT 112

Qy 121 TTVTSS 126  
 Db 113 LTVTSS 118

RESULT 8  
 A32483  
 Ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 16-Aug-1996  
 C:Accession: A32483  
 R:Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C.  
 Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989  
 A:Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usi  
 A:Reference number: A32483; MUID:89273586; PMID:2499327  
 A:Accession: A32483  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-142 <LAR>  
 A:Cross-references: UNIPARC:UPI0000176C19; GB:M26463  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:25-108/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 504.5; DB 2; Length 142;  
 Best Local Similarity 78.0%; Pred. No. 2.8e-38;  
 Matches 99; Conservative 11; Mismatches 16; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60  
 Db 11 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 70

Qy 61 AQKQGRVTMTNTSISTAYMELSLRSEDYAVVYCARD-VMTFGGVIVHYGMDVWGQ 119  
 Db 71 AQKQGRVTMTNTSISTAYMELSLRSEDYAVVYCARDVMTFGGVIVHYGMDVWGQ 130

Qy 120 TTVTSS 126  
 Db 131 LTVTSS 137

RESULT 9  
 S49530  
 anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human  
 C:Species: Homo sapiens (man)  
 C>Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 23-Jul-1999  
 C:Accession: S49530  
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.  
 A:Reference number: S48797  
 A:Accession: S49530  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-135 <MAH>  
 A:Cross-references: UNIPARC:UPI00001166FF; EMBL:Z46348; NID:G560839; PIDN:CAA86467.1; PI  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.4%; Score 502; DB 2; Length 135;  
 Best Local Similarity 77.8%; Pred. No. 4.5e-38;  
 Matches 98; Conservative 6; Mismatches 12; Indels 10; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60  
 Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 79

Qy 61 AQKQGRVTMTNTSISTAYMELSLRSEDYAVVYCARDVMTFGGVIVHYGMDVWGQGT 120  
 Db 80 AQKQGRVTMTNTSISTAYMELSLRSEDYAVVYCAR-----ARTGVNYWGQGT 129

Qy 121 TTVTSS 126  
 Db 130 LTVTSS 135

RESULT 10  
 D33548  
 Ig heavy chain V-1 region (W1L2) - human  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
 C:Accession: D33548  
 R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
 A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr  
 A:Reference number: A33548; MUID:89345575; PMID:2503826  
 A:Accession: D33548  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-123 <KIP>  
 A:Cross-references: UNIPARC:UPI0000176909  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 495.5; DB 2; Length 123;  
 Best Local Similarity 75.4%; Pred. No. 1.6e-37;  
 Matches 95; Conservative 13; Mismatches 15; Indels 3; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60  
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60

Qy 61 AQKQGRVTMTNTSISTAYMELSLRSEDYAVVYCARDVMTFGGVIVHYGMDVWGQGT 120  
 Db 119 AQKQGRVTMTNTSISTAYMELSLRSEDYAVVYCARDVMTFGGVIVHYGMDVWGQGT 120

Db 61 AEKFGQGVITRTDTSINTAYMELSLRLSDDTAVYYCAR---ASYCGYDCYFFDYWGQGT 117

QY 121 TTVTVSS 126  
|||||

Db 118 LVTVSS 123

RESULT 11

S36260

Ig heavy chain V region (clone alpha-CEN4-8A) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999

C/Accession: S36260

R/Griffiths, A.D.; Mallmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36256; MUID:93178448; PMID:7679990

A/Accession: S36260

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-129 <GRI>

A/Cross-references: UNIPARC:UPI0000118DBB; EMBL:Z18851; NID:g33124; PIDN:CAA79303.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 493.5; DB 2; Length 129;  
Best Local Similarity 75.0%; Pred. No. 2.5e-37;  
Matches 99; Conservative 9; Mismatches 15; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKKPKASVKSCASGYTFTSYDINVRQATGQGLEWMGMWNPNSGNTGY 60  
|||||

Db 1 QVQLVQSGAEVKKPKASVKSCASGYTFTSYDINVRQAPGQGLEWMGMWISAYNGTNY 60  
|||||

QY 61 AQKFGQGVITRTDTSINTAYMELSLRLSDDTAVYYCARDVMTFGGV-----IVHYGMD 114  
|||||

Db 61 AQKLGQGVITRTDTSINTAYMELSLRLSDDTAVYYCARD---SFGYCSSTSCPYYYMYMD 117  
|||||

QY 115 VMGQGTTVTVSS 126  
|||||

Db 118 VMGKGTTVTVSS 129  
|||||

RESULT 12

S23623

Ig heavy chain V region precursor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C/Accession: S23623

R/Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A/Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from b

A/Reference number: S23623; MUID:92156804; PMID:1740665

A/Accession: S23623

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-171 <OLE>

A/Cross-references: UNIPARC:UPI0000115F93; EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.9%; Score 492; DB 2; Length 171;  
Best Local Similarity 74.6%; Pred. No. 4.5e-37;  
Matches 94; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPKASVKSCASGYTFTSYDINVRQATGQGLEWMGMWNPNSGNTGY 60  
|||||

Db 20 QVQLVQSGAEVKKPKASVKSCASGYTFTAYQMHVVRQAPGQGLEWMGMWNPNSGNTGY 79  
|||||

QY 61 AQKFGQGVITRTDTSINTAYMELSLRLSDDTAVYYCARDVMTFGGVIVHYGMDVMGQGT 120  
|||||

Db 80 GQKFGQGVITRTDTSINTAYMELSLRLSDDTAVYYCAIEFYDGSDLKPSDVFIDWGQGT 139  
|||||

QY 121 TTVTVSS 126  
|||||

Db 140 MVTVSS 145

## RESULT 13

PH1666

Ig heavy chain V region (clone 6C9) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996

C/Accession: PH1666

R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo

A/Reference number: PH1642; MUID:93301610; PMID:8315388

A/Accession: PH1666

A/Molecule type: mRNA

A/Residues: 1-118 &lt;HIL&gt;

A/Cross-references: UNIPARC:UPI0000176BE7

A/Experimental source: B cell

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 73.0%; Score 486; DB 2; Length 118;

Best Local Similarity 79.3%; Pred. No. 1.1e-36;

Matches 96; Conservative 8; Mismatches 11; Indels 6; Gaps 2;

QY 9 AEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRV 68  
|||||Db 1 AEVKKPGASVKVSKASGYTFTSYAMHVVRQAPGQRLWGMWINAGNGNTKYAQKFGQGRV 60  
|||||QY 69 TMTRTNTSISTAYMELSLRLSDDTAVYYCARDVMTFGGVI---VHYGMDVMGQGTTVTVS 125  
|||||Db 61 TITRDTASTAYMELSLRLSDDTAVYYCAR---VTLDGKIFYYIYGYGMDVMGQGTTVTVS 117  
|||||

QY 126 S 126

Db 118 S 118

## RESULT 14

S19665

Ig heavy chain V region (alpha-phox15) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 20-Jun-2000

C/Accession: S19665; S24442

R/Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,

J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph

A/Reference number: S19663; MUID:92085276; PMID:1748994

A/Accession: S19665

A/Molecule type: mRNA

A/Residues: 1-124 &lt;VAR&gt;

A/Cross-references: UNIPARC:UPI0000176B80; EMBL:X61647.

R/Jones, P.T.

submitted to the EMBL Data Library, October 1991

A/Reference number: S24442

A/Accession: S24442

A/Molecule type: mRNA

A/Residues: 1-40, 'GUSGWDGSGALTMTWTQILDK', 61-118, 'T', 120-124 &lt;JON&gt;

A/Cross-references: UNIPARC:UPI0000115FEG; EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID

A/Note: the difference for residues 41-60 results from misplacement of 10 bases in the s

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 73.0%; Score 486; DB 2; Length 124;

Best Local Similarity 75.4%; Pred. No. 1.1e-36;

Matches 95; Conservative 11; Mismatches 18; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVKKPKASVKVSKASGYTFTSYDINVRQATGQGLEWMGMWNPNSGNTGY 60  
|||||

```
Db 1 QVQLVQSGAEVKPKGASVKSCASGYTFSTSYGISLVWRQAPGGGLEWMGMSAYNGNTKY 60
QY 61 AQKFGQGRVTWTRNTSISTAYMELSSLRSEDTAVYCARDVMTITFGGVIHYGMDVMGQGT 120
Db 61 AQKLGQGRVTWTRNTSISTAYMELSSLRSEDTAVYCARDVMTITFGGVIHYGMDVMGQGT 120
QY 121 TTVVSS 126
Db 119 LTVVSS 124
```

## RESULT 15

```
PH0961
IG heavy chain V region (G6+ T-L33) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0961
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0961
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-119 <MAR>
A:Cross-references: UNIPARC:UPI0000176CES
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-107/Region: complementarity-determining 3
```

```
Query Match 71.4%; Score 475.5; DB 2; Length 119;
Best Local Similarity 76.2%; Pred. No. 9.3e-36;
Matches 96; Conservative 7; Mismatches 16; Indels 7; Gaps 1;
```

```
QY 1 QVQLVQSGAEVKPKGASVKSCASGYTFSTSYDINWRQATGGGLEWMGMNPNNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGSSVKSCASGTFSSYALISWRQAPGGGLEWMGGIIPFGTANY 60
QY 61 AQKFGQGRVTWTRNTSISTAYMELSSLRSEDTAVYCARDVMTITFGGVIHYGMDVMGQGT 120
Db 61 AQKFGQGRVTITADESTSTAYMELSSLRSEDTAVYCARDVMTITFGGVIHYGMDVMGQGT 113
QY 121 TTVVSS 126
Db 114 TTVVSS 119
```

Search completed: April 25, 2007, 04:06:40  
Job time : 9.61017 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 86 Seconds  
(without alignments)  
1574.822 Million cell updates/sec

Title: US-10-665-383-22  
Perfect score: 666  
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....VIVHGMVDVWGQGTIVTVSS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_8.4.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517	77.6	159	2	Q96QSO_HUMAN
2	495.5	74.4	125	2	Q9UL95_HUMAN
3	488.5	73.3	244	2	Q65ZC8_HUMAN
4	480.5	72.1	119	2	Q9UL94_HUMAN
5	479	71.9	124	2	Q9UL92_HUMAN
6	459	68.9	518	2	Q6N030_HUMAN
7	453	68.0	498	2	Q6N041_HUMAN
8	452.5	67.9	497	2	Q8WY24_HUMAN
9	431.5	67.8	500	2	Q6N091_HUMAN
10	451	67.7	147	1	HVIC_HUMAN
11	441.5	66.3	119	2	Q9GYZ2_MOUSE
12	441	66.2	500	2	Q9BRV0_HUMAN
13	437	65.6	117	1	HV1B_HUMAN
14	437	65.6	117	1	HVIC_HUMAN
15	429	64.4	469	2	Q7Z7P5_HUMAN
16	425	63.8	475	2	Q6N095_HUMAN
17	420.5	63.1	458	2	Q5BZ22_RAT
18	417.5	62.7	480	2	Q6P089_HUMAN
19	417.5	62.7	519	2	Q5EBM2_HUMAN
20	417	62.6	617	2	Q4KML5_MOUSE
21	415.5	62.4	157	2	Q95978_HUMAN
22	412	61.9	145	2	Q92409_MOUSE
23	408.5	61.3	117	2	Q9QXE9_MOUSE
24	408.5	61.3	458	2	Q5BK05_RAT
25	408	61.3	116	2	Q9UL89_HUMAN
26	406.5	61.0	481	2	Q91WT1_MOUSE
27	405.5	60.9	120	1	HV03_MOUSE
28	405	60.8	590	2	Q4V9V8_MOUSE
29	404.5	60.7	150	2	Q9Y298_HUMAN
30	404	60.7	145	2	Q92406_MOUSE
31	402.5	60.4	134	2	Q65ZK6_MOUSE

32	401.5	60.3	146	2	Q924Q3_MOUSE
33	401.5	60.3	480	2	Q6PJF1_HUMAN
34	400.5	60.1	147	2	Q925S3_MOUSE
35	400	60.1	141	2	Q924Q4_MOUSE
36	399.5	60.0	117	2	Q9QXF0_MOUSE
37	399	59.9	145	2	Q924R1_MOUSE
38	398.5	59.8	117	1	HVIC_MOUSE
39	398.5	59.8	208	2	Q6ZP87_HUMAN
40	398	59.8	463	2	Q99LC4_MOUSE
41	398	59.8	591	2	Q4QW0_RAT
42	398	59.8	613	2	Q8VCX7_MOUSE
43	397.5	59.7	117	1	HVIC_MOUSE
44	396	59.5	120	2	Q6NSA4_HUMAN
45	396	59.5	145	2	Q924R4_MOUSE

## ALIGNMENTS

RESULT 1  
Q96QSO\_HUMAN PRELIMINARY; PRT; 159 AA.  
AC Q96QSO;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 18-APR-2006, entry version 21.  
DE Putative matrix cell adhesion molecule-3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Tilson M.D.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL; AY039025; AAKG2649.1; -; mRNA.  
DR HSSP; P01869; IAE6.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig sub.  
DR InterPro; IPR013106; Ig\_V-set.  
DR InterPro; IPR003596; Ig\_V-set\_sub.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain.  
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 77.6%; Score 517; DB 2; Length 159;  
Best Local Similarity 75.4%; Pred No. 2.2e-45;  
Matches 98; Conservative 16; Mismatches 12; Indels 4; Gaps 1;  
Qy 1 QVQLVQSGAEVKKPGASVKSKASGYTFTSYDINWVRQATQGLEWMGMNPNSGNTGY 60  
Db 20 QVQLVQSGAEVKKPGASVKSKASGYTFTSYNYMNVVRQAPQGPEWGMVINPSSGGSARY 79  
Qy 61 AQKQGRVTMTNTSISTAYNELSLRSEDATVYVCARDVMITFGVI-----VHYGMDVW 116  
Db 80 SQKQGRLLTTRDSTSTVYMDLSRLRSDTAVYFCAREMEITFGGAVSKGFFYYGMDVW 139  
Qy 117 GQGTIVTVSS 126  
Db 140 GQGTIVTVSS 149

RESULT 2  
Q9UL95\_HUMAN PRELIMINARY; PRT; 125 AA.  
ID Q9UL95\_HUMAN

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AC Q9UL95;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 2.
DT 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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CC -----
DR EMBL; AF035019; AAD56255.1; -; mRNA.
DR HSSP; P01751; INQB.
DR SMR; Q9UL95; 1-122.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW immunoglobulin domain.
FT NON_TER 1
FT NON_TER 125
FT NON_TER 1
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 74.4%; Score 495.5; DB 2; Length 125;
Best Local Similarity 76.6%; Pred. No. 2.9e-43;
Matches 98; Conservative 9; Mismatches 16; Indels 5; Gaps 2;

Qy 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Dy :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGMNPNSGNTNY 60

Qy 61 AQRFGQGVTTMTRTSTISAYMELSLRSEDATVYICARDVMITFGGVIVHYGMDVWGQ 118
Dy :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQRFGQGVTTMTRTSTISAYMELSLRSEDATVYICARS---QGGGRIAAAGDAFDIWGQ 117

Qy 119 GTTVTVSS 126
Dy |||:|||||
Db 118 GTTVTVSS 125

RESULT 3
Q65ZC8 HUMAN
ID Q65ZC8_HUMAN PRELIMINARY; PRT; 244 AA.
AC Q65ZC8;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 18-APR-2006, entry version 10.
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;

Query Match 74.4%; Score 495.5; DB 2; Length 125;
Best Local Similarity 76.6%; Pred. No. 2.9e-43;
Matches 98; Conservative 9; Mismatches 16; Indels 5; Gaps 2;

Qy 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Dy :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGMNPNSGNTNY 60

Qy 61 AQRFGQGVTTMTRTSTISAYMELSLRSEDATVYICARDVMITFGGVIVHYGMDVWGQ 118
Dy :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQRFGQGVTTMTRTSTISAYMELSLRSEDATVYICARS---QGGGRIAAAGDAFDIWGQ 117

Qy 119 GTTVTVSS 126
Dy |||:|||||
Db 118 GTTVTVSS 125

RESULT 4
Q9UL94 HUMAN
ID Q9UL94_HUMAN PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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CC -----
DR EMBL; AF035020; AAD56256.1; -; mRNA.
DR HSSP; P01751; INQB.
DR SMR; Q9UL94; 1-116.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
RT NON_TER 1
RT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 73.3%; Score 488.5; DB 2; Length 244;
Best Local Similarity 74.6%; Pred. No. 3.3e-42;
Matches 94; Conservative 14; Mismatches 13; Indels 5; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Dy :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKPGDSVKVSCKASGYTFSHYMHWVRQAPGQGLEWMGWIDPNNGDTRF 60

Qy 61 AQRFGQGVTTMTRTSTISAYMELSLRSEDATVYICARDVMITFGGVIVHYGMDVWGQ 120
Dy :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQRFGQGVTTMTRTSTISAAVMEVSRSLRSDATVYVCARE---GTGSAIYGMVDVWGQ 115

Qy 121 TTVTVSS 126
Dy |||:|||||
Db 116 TTVTVSS 121
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RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
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CC -----
DR EMBL; Y13057; CAA73500.1; -; mRNA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW immunoglobulin domain.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 73.3%; Score 488.5; DB 2; Length 244;
Best Local Similarity 74.6%; Pred. No. 3.3e-42;
Matches 94; Conservative 14; Mismatches 13; Indels 5; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Dy :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKPGDSVKVSCKASGYTFSHYMHWVRQAPGQGLEWMGWIDPNNGDTRF 60

Qy 61 AQRFGQGVTTMTRTSTISAYMELSLRSEDATVYICARDVMITFGGVIVHYGMDVWGQ 120
Dy :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQRFGQGVTTMTRTSTISAAVMEVSRSLRSDATVYVCARE---GTGSAIYGMVDVWGQ 115

Qy 121 TTVTVSS 126
Dy |||:|||||
Db 116 TTVTVSS 121

RESULT 4
Q9UL94 HUMAN
ID Q9UL94_HUMAN PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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CC -----
DR EMBL; AF035020; AAD56256.1; -; mRNA.
DR HSSP; P01751; INQB.
DR SMR; Q9UL94; 1-116.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
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KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 72.1%; Score 480.5; DB 2; Length 119;
Best Local Similarity 75.4%; Pred. No. 1e-41;
Matches 95; Conservative 11; Mismatches 13; Indels 7; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKSCASGTYFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 60
1 EQVLVSGAEVKKPGASVKSCASGTYFTCYGHHWVRQAPQGQLEWGMWNPNSWTNY 60
Qy 61 AQKQGRVTMTTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 120
61 AQKQGRVTMTKDTISISTAYMELSLRSLSDDTAVYYCARG-----GGRGLWF--DPWGQGT 113

Qy 121 TTVTSS 126
Db :||||:
114 LVTSS 119

RESULT 5
Q9UL92 HUMAN PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 18-APR-2006, entry version 22.
OS Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
NP NUCLEOTIDE SEQUENCE.
TX TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Meves H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBS databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC
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CC
DR EMBL; BX640724; CAE45841.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR LinkHub; Q6N030; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SQ SEQUENCE 518 AA; 57020 MW; 93B5F98613BF6382 CRC64;

Query Match 68.9%; Score 459; DB 2; Length 518;
Best Local Similarity 73.0%; Pred. No. 9e-39;
Matches 92; Conservative 10; Mismatches 20; Indels 4; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKSCASGTYFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 60
20 QVHLVQSGAEVKKPGASVKSCASGTYFTNHNWVRQAPQGQLEWGMWNPNSGNTKY 79
Qy 61 AQKQGRVTMTTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 120
80 SQKQGRVTITRDITTTTAYMDLSSLRSEDATVYVWCDAP---QGVTTTY-FDYWGQGT 135

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Qy	121	TVTVSS 126
Dd	136	LTVTSS 141
RESULT 7		
Q6N041_HUMAN	PRELIMINARY;	PRT; 498 AA.
ID Q6N041	HUMAN	AC
DT 05-JUL-2004,	integrated into UniProtKB/TrEMBL.	
DT 05-JUL-2004,	sequence version 1.	
DT 18-APR-2006,	entry version 13.	
DE Hypothetical protein DKFZp686O16217 (Fragment).		
GN Name=DKFP686O16217;		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;		
OC Catarrhini; Homnidae; Homo.		
NCBI_TaxID=9606;		
[1]		
NUCLEOTIDE SEQUENCE.		
DR HSP; P01751; IAGW.		
DR TISSUE=Human rectum tumor;		
RG The German Human cDNA Consortium;		
RA Foustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,		
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;		
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.		
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-----		
EMBL; BX640710; CAE45829.1; -; mRNA.		
DR HSP; P01751; IAGW.		
DR SMR; Q6N041; 268-476.		
DR InterPro; IPR007110; Ig-like.		
DR InterPro; IPR003597; Ig_C1-set.		
DR InterPro; IPR003006; Ig_MHC.		
DR InterPro; IPR003599; Ig_sub.		
DR InterPro; IPR013106; Ig V-set.		
DR InterPro; IPR003596; Ig_V-set_sub.		
DR Pfam; PF07654; Cl-set; 2.		
DR SMART; SM00407; IGV; 1.		
DR SMART; SM00407; IGV; 2.		
DR SMART; SM00406; IGV; 1.		
DR PROSITE; PS00835; IG LIKE; 4.		
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.		
KW Hypothetical protein; Immunoglobulin domain; Repeat.		
FT NON_TER 1		
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;		
Query Match 68.0%; Score 453; DB 2; Length 498;		
Best Local Similarity 70.5%; Pred. No. 3.6e-38;		
Matches 91; Conservative 11; Mismatches 19; Indels 8; Gaps 2;		
Qy	1	QVQLVQSGLAEVKKPGASVKSCASGYTFSTYDINVRQATGCGLEWMGMNPNSGNTGY 60
Dd	35	QVQLVQSGADVKKPKGASVKSCASGYTFNYFFHWVQAQPGQPENWGMINPRDGSTKY 94
-----		
Qy	61	AQKFGQRVTMTNTSISTAYMELSLRSIEDTAIVYCARDVMITFG--GVLVHYGMDVWG 117
Dd	95	AQRFQGRVSMTRDTSTIYMELSLRSIEDTAMFFCAR-----AGPGYGTSASYFYDWG 149
-----		
Qy	118	OQTTLTVSS 126
Dd	150	OQTTLTVSS 158
RESULT 8		
Q8WY24_HUMAN	PRELIMINARY;	PRT; 497 AA.
ID Q8WY24	HUMAN	AC
DT 01-MAR-2002,	integrated into UniProtKB/TrEMBL.	
DT 01-MAR-2002,	sequence version 1.	

RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
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CC -----  
CC EMBL: BX640625; CA645779.1; -, mRNA.  
DR HSPF; P01751; 1A6W.  
DR SMR; Q6N091; 270-478.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig C1-set.  
DR InterPro; IPR03006; Ig MHC.  
DR InterPro; IPR003599; Ig sub.  
DR InterPro; IPR013106; Ig V-set.  
DR InterPro; IPR003596; Ig V-set\_sub.  
DR Pfam; PF07654; C1-set; 2.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00407; IGc1; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.  
KW Hypothetical protein; Immunoglobulin domain; Repeat.  
FT NON TER 1  
SQ SEQUENCE 500 AA; 54160 MW; 3C423A17D65A4184 CRC64;  
Query Match 67.8%; Score 451.5; DB 2; Length 500;  
Best Local Similarity 70.6%; Pred. No. 5.2e-38;  
Matches 89; Conservative 11; Mismatches 23; Indels 3; Gaps 1;  
Qy 1 QVQLVQSGAEVKPGASVKSCASGYTFSTVDINVRQATGQGLEWMGNPNPNSGNTGY 60  
Db 38 QVQLVQSGAEVKPGASVKSCASGYTFSDHSITLRLQAPGQGLEWIGMISAYSGQTY 97  
Qy 61 AQKPGQVTRTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQT 120  
Db 98 AQNLQGRVTMTDTSTAYMELSLRSDDTAVYCAKQDSYT---TIPDAFHGQGT 154  
Qy 121 TTVTVSS 126  
Db 155 MVTVSS 160  
RESULT 10  
HV1C\_HUMAN STANDARD; PRT; 147 AA.  
AC P01744;  
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
DT 01-DEC-2000, sequence version 2.  
DT 30-MAY-2006, entry version 47.  
DE Ig heavy chain V-I region ND precursor (Fragments).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
OC Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83065234; PubMed=6815656;  
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
RA Bell L.O., Gould H.J.;  
RT "Cloning and sequence determination of the gene for the human  
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).  
RN [2]  
RP PROTEIN SEQUENCE OF 20-147.  
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RL (in) Bach M.K. (eds.);  
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,

RL Marcel Dekker, New York (1978).  
CC -!- MISCELLANEOUS: This epsilon chain was isolated from a myeloma  
CC protein.  
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC HSPF; P01751; INQB.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig sub.  
DR InterPro; IPR003596; Ig V-set\_sub.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region; Pyroglutamate carboxylic acid; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 147  
FT 19 Ig heavy chain V-I region ND.  
FT /FTID=PRO\_0000015246.  
FT 20 Ig-like.  
FT DOMAIN 20 131  
FT MOD RES 20 20  
FT DISULFID 41 115  
FT CONFLICT 21 21  
FT CONFLICT 53 54  
FT CONFLICT 67 68  
FT CONFLICT 125 125  
FT NON TER 147  
SQ SEQUENCE 147 AA; 16496 MW; 948F9F72A5366C20 CRC64;  
Query Match 67.7%; Score 451; DB 1; Length 147;  
Best Local Similarity 67.2%; Pred. No. 1.5e-38;  
Matches 86; Conservative 15; Mismatches 25; Indels 2; Gaps 1;  
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Db 20 QVQLVQSGAEVKPGASVKSCASGYTFIDSYTHWIRQAPGQGLEWGNINPNSGNTY 79  
Qy 61 AQKPGQVTRTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQT 118  
Db 80 APFQGRVTMTDASFSFAYMDLSRSDSDSAVFCAKSDPWSDYNYFDYSYTLDVWGQ 139  
Qy 119 GTTVTVSS 126  
Db 140 GTTVTVSS 147  
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AC Q9GYZ2;  
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2001, sequence version 1.  
DT 18-APR-2006, entry version 22.  
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy  
DE chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Murioidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Song X.T., Feng Z.Q., Guan X.H.;  
RT "Amplification, cloning and sequence analysis of the heavy chain  
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of  
RT Schistosoma japonicum.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; AF282622; AAC01452.1; -; mRNA.  
 DR HSSP; P01753; 1A6W.  
 DR SMR; Q9GYZ2; 1-119.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003599; Ig sub.  
 DR InterPro; IPR013106; Ig V-set.  
 DR InterPro; IPR003596; Ig\_V-set\_sub.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS0835; IG LIKE; 1.  
 KW Immunoglobulin domain.  
 FT NON\_TER 1 119  
 FT NON\_TER 119 119  
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 Best Local Similarity 67.4%; Pred. No. 1.1e-37;  
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 Db 1 QVQLVESGAERKPGASVRSCKASGYTFTGYVMNVRQAPGHGLEWIGYINPSRGYTN 60  
 Qy 61 AQKQGRVTMTNTSISTAYMELSLRSDTAVYICAR---DVMTFGGVIVHYGMDVWG 117  
 Db 61 NQKFKDVTMTTKDSFTAYMDLRSLRSADSAVYICARYDD-----HYCLDYWG 110  
 Qy 118 GTTIVTVSS 126  
 Db 111 QGTVTVSS 119  
 RESULT 12  
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 ID Q9BRV0\_HUMAN PRELIMINARY; PRT; 500 AA.  
 AC Q9BRV0;  
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2001, sequence version 1.  
 DT 25-JUL-2006, entry version 36.  
 DE IGHAI protein.  
 GN Name=IGHAI;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
 OC Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Prostate;  
 RG Mammalian Gene Collection Program Team;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulliahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Viallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Prostate;  
 RG NIH MGC Project;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL; BC005951; AA05951.1; -; mRNA.  
 DR HSSP; P01876; 10W0.  
 DR SMR; Q9BRV0; 25-300, 270-478.  
 DR Ensembl; ENSG00000130076; Homo sapiens.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0016020; C: membrane; IEA.  
 DR GO; GO:0030106; F: MHC class I receptor activity; IEA.  
 DR GO; GO:0019883; P: antigen presentation, endogenous antigen; IEA.  
 DR GO; GO:0019885; P: antigen processing, endogenous antigen via . . .; IEA.  
 DR InterPro; IPR013151; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_C1-set.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003599; Ig sub.  
 DR InterPro; IPR013106; Ig V-set.  
 DR InterPro; IPR003596; Ig\_V-set\_sub.  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IGc1; 2.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS0835; IG LIKE; 4.  
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 Best Local Similarity 68.0%; Pred. No. 6.4e-37;  
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 Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLGWGMNPNSTGY 60  
 Db 20 QVHLVQSGAEVMSFGASVRSCKTSGYAFHTYSIIWVRQAPQGLGWGMNPNSTTRF 79  
 Qy 61 AQKQGRVTMTNTSISTAYMELSLRSDTAVYICARDV--MITFGGVIVHYGMDVWGQ 118  
 Db 80 AKKQGRVTLTDTSTVTVMELSLRSDTAVYICARRYCSYSSCONDYIIYYMDVWGK 139  
 Qy 119 GTTIVTVSS 126  
 Db 140 GTTIVTVSS 147  
 RESULT 13  
 HV1B HUMAN  
 ID HV1B\_HUMAN STANDARD; PRT; 117 AA.  
 AC P01743;  
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot..  
 DT 21-JUL-1986, sequence version 1.  
 DT 30-MAY-2006, entry version 43.  
 DT Ig heavy chain V-I region HG3 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
 OC Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=83144028; PubMed=6298778;  
 RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;  
 RT "Evolutionary aspects of immunoglobulin heavy chain variable region  
 (VH) gene subgroups.";  
 Proc. Natl. Acad. Sci. U.S.A. 80:855-859 (1983).

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CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC -----
DR EMBL; J00240; AAS52988.1; -; Genomic_DNA.
DR PIR; A02024; HVHUG.
DR HSSP; P01751; INOB.
DR LinkHub; P01743; 20-117.
DR LinkHub; P01743; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR013106; Ig V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
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FT DOMAIN 20 >117 Ig heavy chain V-I region HG3.
FT NON_TER 117
FT SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
FT -----
Query Match 65.6%; Score 437; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3.2e-37;
Matches 84; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGY 60
DB 20 QVQLVQSGAEVKPKGASVKSCASGYTFNYYMHVWRQAPQGLEWGIINPSGGSITSY 79
QY 61 AQKFGQRTVTRNTSISTAYMELSLRSRSDTAVYYCAR 98
DB 80 AQKFGQRTVTRNTSISTAYMELSLRSRSDTAVYYCAR 117

RESULT 14
HV1G HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1991, sequence version 1.
DT 30-MAY-2006, entry version 38.
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus.";
RL EMBO J. 7:1047-1051 (1988).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 20-116.
RX MEDLINE=93209281; PubMed=7681398;
RA Mariette X., Teapis A., Brouet J.C.;
RT "Nucleotide sequence analysis of the variable domains of four human
RT monoclonal IgM with an antibody activity to myelin-associated
RT glycoprotein.";
RL Eur. J. Immunol. 23:846-851 (1993).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC -----

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CC EMBL; X07448; -; NOT ANNOTATED_CDS; Genomic_DNA.
DR PIR; S00476; HVH035.
DR HSSP; P01751; INOB.
DR SMR; P23083; 20-117.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR LinkHub; P23083; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 >117 Ig heavy chain V-I region V35.
FT NON_TER 117
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Best Local Similarity 85.7%; Pred. No. 3.2e-37;
Matches 84; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGY 60
DB 20 QVQLVQSGAEVKPKGASVKSCASGYTFTGYMHVWRQAPQGLEWGIINPSGGSITSY 79
QY 61 AQKFGQRTVTRNTSISTAYMELSLRSRSDTAVYYCAR 98
DB 80 AQKFGQRTVTRNTSISTAYMELSLRSRSDTAVYYCAR 117

RESULT 15
Q7Z7P5 HUMAN PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 27-JUN-2006, entry version 25.
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC051328; AAH51328.1; -; mRNA.
DR HSSP; P01857; 1HZH
DR SMR; Q727P5; 20-469.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_v-set.
DR InterPro; IPR003596; Ig_v-set_sub.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Immunoglobulin domain; Membrane; Repeat; Transmembrane.
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Query Match 64.4%; Score 429; DB 2; Length 469;
Best Local Similarity 65.9%; Pred. No. 1.le-35;
Matches 83; Conservative 15; Mismatches 22; Indels 6; Gaps 1;

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QY 121 TTVTVSS 126
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Db 134 LTVTVSS 139

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Search completed: April 25, 2007, 04:06:37  
Job time : 86.7797 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:06:51 ; Search time 16 Seconds  
(without alignments)  
696.311 Million cell updates/sec

Title: US-10-665-383-22

Perfect score: 666

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....VIVHGMVWGQGTITVWS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SID33/ptodata/2/iaa/5 COMB.pep.\*
- 2: /EMC\_Celerra\_SID33/ptodata/2/iaa/6 COMB.pep.\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/iaa/7 COMB.pep.\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/iaa/8 COMB.pep.\*
- 5: /EMC\_Celerra\_SID33/ptodata/2/iaa/9 COMB.pep.\*
- 6: /EMC\_Celerra\_SID33/ptodata/2/iaa/RE COMB.pep.\*
- 7: /EMC\_Celerra\_SID33/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	526	79.0	120	2	US-09-025-769B-36
2	526	79.0	120	2	US-09-025-769B-59
3	526	79.0	120	2	US-09-490-070A-36
4	526	79.0	120	2	US-09-490-070A-59
5	526	79.0	120	2	US-09-490-153-36
6	526	79.0	120	2	US-09-490-153-59
7	526	79.0	120	2	US-09-490-324-36
8	526	79.0	120	2	US-09-490-324-59
9	524.5	78.8	117	2	US-09-025-769B-22
10	524.5	78.8	117	2	US-09-490-070A-22
11	524.5	78.8	117	2	US-09-490-153-22
12	524.5	78.8	117	2	US-09-490-324-22
13	517	77.6	117	2	US-08-545-809A-96
14	517	77.6	117	2	US-09-515-697-96
15	509.5	76.5	470	2	US-09-859-053-28
16	508	76.3	96	2	US-10-194-975-3
17	498.5	74.8	123	2	US-10-330-613A-21
18	497.5	74.7	123	1	US-08-477-877B-21
19	497.5	74.7	123	1	US-08-472-281A-94
20	497.5	74.7	123	1	US-08-477-989B-94
21	497.5	74.7	123	2	US-09-462-140D-102
22	497.5	74.7	123	2	US-09-462-140D-105
23	491.5	73.8	125	2	US-09-199-149-3
24	491.5	73.8	129	1	US-08-561-521-45
25	491.5	73.8	129	2	US-08-525-539A-77
26	491.5	73.8	129	5	PCT-US95-01219-45

27 484.5 72.7 119 1 US-08-561-521-10 Sequence 10, Appl  
28 484.5 72.7 119 5 PCT-US95-01219-10 Sequence 10, Appl  
29 482 72.4 128 1 US-08-202-047-22 Sequence 22, Appl  
30 482 72.4 128 2 US-08-964-690-22 Sequence 22, Appl  
31 481.5 72.3 119 2 US-09-438-954-41 Sequence 41, Appl  
32 478 71.8 139 1 US-08-253-877C-19 Sequence 19, Appl  
33 478 71.8 139 1 US-08-452-164A-19 Sequence 19, Appl  
34 478 71.8 139 2 US-08-603-024-18 Sequence 18, Appl  
35 478 71.8 139 2 US-08-450-809-14 Sequence 14, Appl  
36 474 71.2 118 3 US-09-875-221B-13 Sequence 13, Appl  
37 470.5 70.6 119 1 US-08-300-386A-65 Sequence 65, Appl  
38 470.5 70.6 119 2 US-08-931-845-65 Sequence 65, Appl  
39 470.5 70.6 119 5 PCT-US95-11235-65 Sequence 65, Appl  
40 470.5 70.6 121 1 US-08-202-047-23 Sequence 23, Appl  
41 470.5 70.6 121 2 US-08-964-690-23 Sequence 23, Appl  
42 469.5 70.5 123 1 US-08-482-882-86 Sequence 86, Appl  
43 469.5 70.5 123 1 US-08-483-389-86 Sequence 86, Appl  
44 469.5 70.5 123 1 US-08-487-113D-86 Sequence 86, Appl  
45 469.5 70.5 123 1 US-08-473-503-86 Sequence 86, Appl

#### ALIGNMENTS

RESULT 1  
US-09-025-769B-36  
; Sequence 36, Application US/09025769B  
; Patent No. 630064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthum, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-36  
Query Match 79.0%; Score 526; DB 2; Length 120;  
Best Local Similarity 83.3%; Pred. No. 5.5e-45;

Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

Qy 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60  
Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60

Qy 61 AQKFGQVMTTRNTSISTAYMELSSLRSEDPAVYICARDVMITFGGVIVHYGMDVWGQGT 120  
Db 61 AQKFGQVMTTRNTSISTAYMELSSLRSEDPAVYICARDVMITFGGVIVHYGMDVWGQGT 114

Qy 121 TVTVSS 126  
Db 115 LVTVSS 120

RESULT 2  
US-09-025-769B-59  
; Sequence 59, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-59

Query Match 79.0%; Score 526; DB 2; Length 120;  
Best Local Similarity 83.3%; Pred. No. 5.5e-45;  
Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

Qy 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60  
Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60

Qy 61 AQKFGQVMTTRNTSISTAYMELSSLRSEDPAVYICARDVMITFGGVIVHYGMDVWGQGT 120  
Db 61 AQKFGQVMTTRNTSISTAYMELSSLRSEDPAVYICARDVMITFGGVIVHYGMDVWGQGT 114

Qy 121 TVTVSS 126  
Db 115 LVTVSS 120

RESULT 3  
US-09-490-070A-36  
; Sequence 36, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-490-070A-36

Query Match 79.0%; Score 526; DB 2; Length 120;  
Best Local Similarity 83.3%; Pred. No. 5.5e-45;  
Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

Qy 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60  
Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60

Qy 61 AQKFGQVMTTRNTSISTAYMELSSLRSEDPAVYICARDVMITFGGVIVHYGMDVWGQGT 120  
Db 61 AQKFGQVMTTRNTSISTAYMELSSLRSEDPAVYICARDVMITFGGVIVHYGMDVWGQGT 114

RESULT 4  
US-09-490-070A-59

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; Sequence 59, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-070A-59
Query Match 79.0%; Score 526; DB 2; Length 120;
Best Local Similarity 83.3%; Pred. No. 5.5e-45;
Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;
QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQAPGQGLEWGMWNPNSGNTY 60
QY 61 AOKFQGRVTMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFQGRVTMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 115 LVTVSS 120
RESULT 5
US-09-490-153-36
; Sequence 36, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-153-36
Query Match 79.0%; Score 526; DB 2; Length 120;
Best Local Similarity 83.3%; Pred. No. 5.5e-45;
Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;
QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQAPGQGLEWGMWNPNSGNTY 60
QY 61 AOKFQGRVTMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFQGRVTMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 115 LVTVSS 120
RESULT 6
US-09-490-153-59
; Sequence 59, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
```

/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10021  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/490,153  
/ FILING DATE: 24-Jan-2000  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/025,769B  
/ FILING DATE: 18-FEB-1998  
/ APPLICATION NUMBER: EP 95 11 3021.0  
/ FILING DATE: 18-AUG-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: James F. Haley, Jr., Esq.  
/ REGISTRATION NUMBER: 27,794  
/ REFERENCE/DOCKET NUMBER: MORPHO/5  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212)596-9000  
/ TELEFAX: (212)596-9090  
/ LENGTH: 120 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
/ US-09-490-153-59  
/ Query Match 79.0%; Score 526; DB 2; Length 120;  
/ Best Local Similarity 83.3%; Pred. No. 5.5e-45;  
/ Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;  
/ QY 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60  
/ Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQAPCGGLEWGMWNPNSGNTNY 60  
/ QY 61 AQKFGQRTVMTNTSISTAYMELSLRSSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120  
/ Db 61 AQKFGQRTVMTNTSISTAYMELSLRSSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120  
/ QY 121 TVTVSS 126  
/ Db 115 LVTVSS 120  
/ RESULT 7  
/ US-09-490-324-36  
/ Sequence 36, Application US/09490324  
/ Patent No. 6828422  
/ GENERAL INFORMATION:  
/ APPLICANT: Knappik, Achim  
/ Pack, Peter  
/ Ilag, Vic  
/ Ge, Liming  
/ Moroney, Simon  
/ Plueckthun, Andreas  
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries  
/ NUMBER OF SEQUENCES: 373  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
/ STREET: 1251 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10021  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/490,324  
/ FILING DATE: 24-Jan-2000  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/025,769  
/ FILING DATE: 18-FEB-1998  
/ APPLICATION NUMBER: EP 95 11 3021.0  
/ FILING DATE: 18-AUG-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: James F. Haley, Jr., Esq.  
/ REGISTRATION NUMBER: 27,794  
/ REFERENCE/DOCKET NUMBER: MORPHO/5  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212)596-9000  
/ TELEFAX: (212)596-9090  
/ INFORMATION FOR SEQ ID NO: 36:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 120 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: <unknown>  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
/ US-09-490-324-36  
/ Query Match 79.0%; Score 526; DB 2; Length 120;  
/ Best Local Similarity 83.3%; Pred. No. 5.5e-45;  
/ Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;  
/ QY 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60  
/ Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQAPCGGLEWGMWNPNSGNTNY 60  
/ QY 61 AQKFGQRTVMTNTSISTAYMELSLRSSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120  
/ Db 61 AQKFGQRTVMTNTSISTAYMELSLRSSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120  
/ QY 121 TVTVSS 126  
/ Db 115 LVTVSS 120  
/ RESULT 8  
/ US-09-490-324-59  
/ Sequence 59, Application US/09490324  
/ Patent No. 6828422  
/ GENERAL INFORMATION:  
/ APPLICANT: Knappik, Achim  
/ Pack, Peter  
/ Ilag, Vic  
/ Ge, Liming  
/ Moroney, Simon  
/ Plueckthun, Andreas  
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries  
/ NUMBER OF SEQUENCES: 373  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
/ STREET: 1251 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10021  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/490,324  
/ FILING DATE: 24-Jan-2000  
/ PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-324-59

Query Match          79.0%; Score 526; DB 2; Length 120;
Best Local Similarity 83.3%; Pred. No. 5.5e-45;
Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

Qy 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGMNPNSGNTNY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVMWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVMWGQGT 114

Qy 121 TVTVSS 126
Db 115 LTVSS 120

RESULT 9
US-09-025-769B-22
; Sequence 22, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11-3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-22

Query Match          78.8%; Score 524.5; DB 2; Length 117;
Best Local Similarity 81.7%; Pred. No. 7.5e-45;
Matches 103; Conservative 5; Mismatches 9; Indels 9; Gaps 1;

Qy 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGMNPNSGNTNY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVMWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVMWGQGT 111

Qy 121 TVTVSS 126
Db 112 LTVSS 117

RESULT 10
US-09-490-070A-22
; Sequence 22, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
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Matches	103;	Conservative	5;	Mismatches	9;	Indels	9;	Gaps
QY	1	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVRQATGQGLEWMGMNPNNGNTGY	60					
DB	1	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHVWRQAPGQGLEWMGWINPNNGNTNY	60					
QY	61	AKQFQGRVTMTNTSISTAYMELSLRSDDTAVYYCARDVMTFGGVIVHYGMDVWGQGT	120					
DB	61	AKQFQGRVTMTTRDTSISTAYMELSLRSDDTAVYYCARDVMTFGGVIVHYGMDVWGQGT	111					
QY	121	TVTSS 126						
DB	112	LTVSS 117						
<p>RESULT 12</p> <p>US-09-490-324-22</p> <p>Sequence 22, Application US/09490324</p> <p>Patent No. 6828422</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Knappik, Achim</p> <p>PACK, Peter</p> <p>Ilag, Vic</p> <p>Ge, Liming</p> <p>Moroney, Simon</p> <p>Plueckthun, Andreas</p> <p>TITLE OF INVENTION: Protein/(Poly)peptide libraries</p> <p>NUMBER OF SEQUENCES: 373</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &amp; Neave</p> <p>STREET: 1251 Avenue of the Americas</p> <p>CITY: New York</p> <p>STATE: New York</p> <p>COUNTRY: USA</p> <p>ZIP: 10021</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/490,324</p> <p>FILING DATE: 24-Jan-2000</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/025,769</p> <p>FILING DATE: 18-FEB-1998</p> <p>APPLICATION NUMBER: EP 95 11 3021.0</p> <p>FILING DATE: 18-AUG-1995</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: James F. Haley, Jr., Esq.</p> <p>REGISTRATION NUMBER: 27,794</p> <p>REFERENCE/DOCKET NUMBER: MORPHO/5</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (212)596-9000</p> <p>TELEFAX: (212)596-9090</p> <p>INFORMATION FOR SEQ ID NO: 22:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 117 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: &lt;Unknown&gt;</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: protein</p> <p>SEQUENCE DESCRIPTION: SEQ ID NO: 22:</p> <p>US-09-490-324-22</p>								
<p>Query Match 78.8%; Score 524.5; DB 2; Length 117;</p> <p>Best Local Similarity 81.7%; Pred. No. 7.5e-45;</p> <p>Matches 103; Conservative 5; Mismatches 9; Indels 9; Gaps 1;</p>								
QY	1	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVRQATGQGLEWMGMNPNNGNTGY	60					
DB	1	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHVWRQAPGQGLEWMGWINPNNGNTNY	60					
QY	61	AKQFQGRVTMTNTSISTAYMELSLRSDDTAVYYCARDVMTFGGVIVHYGMDVWGQGT	120					
DB	61	AKQFQGRVTMTTRDTSISTAYMELSLRSDDTAVYYCARDVMTFGGVIVHYGMDVWGQGT	111					
QY	121	TVTSS 126						
DB	112	LTVSS 117						
<p>RESULT 11</p> <p>US-09-490-153-22</p> <p>Sequence 22, Application US/09490153</p> <p>Patent No. 6708484</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Knappik, Achim</p> <p>PACK, Peter</p> <p>Ilag, Vic</p> <p>Ge, Liming</p> <p>Moroney, Simon</p> <p>Plueckthun, Andreas</p> <p>TITLE OF INVENTION: Protein/(Poly)peptide libraries</p> <p>NUMBER OF SEQUENCES: 373</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &amp; Neave</p> <p>STREET: 1251 Avenue of the Americas</p> <p>CITY: New York</p> <p>STATE: New York</p> <p>COUNTRY: USA</p> <p>ZIP: 10021</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/490,153</p> <p>FILING DATE: 24-Jan-2000</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/025,769B</p> <p>FILING DATE: 18-FEB-1998</p> <p>APPLICATION NUMBER: EP 95 11 3021.0</p> <p>FILING DATE: 18-AUG-1995</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: James F. Haley, Jr., Esq.</p> <p>REGISTRATION NUMBER: 27,794</p> <p>REFERENCE/DOCKET NUMBER: MORPHO/5</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (212)596-9000</p> <p>TELEFAX: (212)596-9090</p> <p>INFORMATION FOR SEQ ID NO: 22:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 117 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: &lt;Unknown&gt;</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: protein</p> <p>SEQUENCE DESCRIPTION: SEQ ID NO: 22:</p> <p>US-09-490-153-22</p>								
<p>Query Match 78.8%; Score 524.5; DB 2; Length 117;</p> <p>Best Local Similarity 81.7%; Pred. No. 7.5e-45;</p> <p>Matches 103; Conservative 5; Mismatches 9; Indels 9; Gaps 1;</p>								

Matches	103;	Conservative	5;	Mismatches	9;	Indels	9;	Gaps
QY	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMGMWNPNSGNTGY	60					
DB	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVWRQAPGQGLEWMGWINPNSGNTNY	60					
QY	61	AKQFGQRTVMTNTSISTAYMELSLRSDDTAVYYCARDVMTFGGVIVHYGMDVWGQGT	120					
DB	61	AKQFGQRTVMTTRDTSISTAYMELSLRSDDTAVYYCARDVMTFGGVIVHYGMDVWGQGT	111					
QY	121	TVTSSS 126						
DB	112	LVTSSS 117						
<p>RESULT 12</p> <p>US-09-490-324-22</p> <p>Sequence 22, Application US/09490324</p> <p>Patent No. 6828422</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Knappik, Achim</p> <p>PACK, Peter</p> <p>Ilag, Vic</p> <p>Ge, Liming</p> <p>Moroney, Simon</p> <p>Plueckthun, Andreas</p> <p>TITLE OF INVENTION: Protein/(Poly)peptide libraries</p> <p>NUMBER OF SEQUENCES: 373</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &amp; Neave</p> <p>STREET: 1251 Avenue of the Americas</p> <p>CITY: New York</p> <p>STATE: New York</p> <p>COUNTRY: USA</p> <p>ZIP: 10021</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/490,324</p> <p>FILING DATE: 24-Jan-2000</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/025,769</p> <p>FILING DATE: 18-FEB-1998</p> <p>APPLICATION NUMBER: EP 95 11 3021.0</p> <p>FILING DATE: 18-AUG-1995</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: James F. Haley, Jr., Esq.</p> <p>REGISTRATION NUMBER: 27,794</p> <p>REFERENCE/DOCKET NUMBER: MORPHO/5</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (212)596-9000</p> <p>TELEFAX: (212)596-9090</p> <p>INFORMATION FOR SEQ ID NO: 22:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 117 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: &lt;Unknown&gt;</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: protein</p> <p>SEQUENCE DESCRIPTION: SEQ ID NO: 22:</p> <p>US-09-490-324-22</p>								
<p>Query Match 78.8%; Score 524.5; DB 2; Length 117;</p> <p>Best Local Similarity 81.7%; Pred. No. 7.5e-45;</p> <p>Matches 103; Conservative 5; Mismatches 9; Indels 9; Gaps 1;</p>								
QY	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVRQATGQGLEWMGMWNPNSGNTGY	60					
DB	1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVWRQAPGQGLEWMGWINPNSGNTNY	60					
QY	61	AKQFGQRTVMTNTSISTAYMELSLRSDDTAVYYCARDVMTFGGVIVHYGMDVWGQGT	120					
DB	61	AKQFGQRTVMTTRDTSISTAYMELSLRSDDTAVYYCARDVMTFGGVIVHYGMDVWGQGT	111					
QY	121	TVTSSS 126						
DB	112	LVTSSS 117						
<p>RESULT 11</p> <p>US-09-490-153-22</p> <p>Sequence 22, Application US/09490153</p> <p>Patent No. 6708484</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Knappik, Achim</p> <p>PACK, Peter</p> <p>Ilag, Vic</p> <p>Ge, Liming</p> <p>Moroney, Simon</p> <p>Plueckthun, Andreas</p> <p>TITLE OF INVENTION: Protein/(Poly)peptide libraries</p> <p>NUMBER OF SEQUENCES: 373</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &amp; Neave</p> <p>STREET: 1251 Avenue of the Americas</p> <p>CITY: New York</p> <p>STATE: New York</p> <p>COUNTRY: USA</p> <p>ZIP: 10021</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/490,153</p> <p>FILING DATE: 24-Jan-2000</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09/025,769B</p> <p>FILING DATE: 18-FEB-1998</p> <p>APPLICATION NUMBER: EP 95 11 3021.0</p> <p>FILING DATE: 18-AUG-1995</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: James F. Haley, Jr., Esq.</p> <p>REGISTRATION NUMBER: 27,794</p> <p>REFERENCE/DOCKET NUMBER: MORPHO/5</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (212)596-9000</p> <p>TELEFAX: (212)596-9090</p> <p>INFORMATION FOR SEQ ID NO: 22:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 117 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: &lt;Unknown&gt;</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: protein</p> <p>SEQUENCE DESCRIPTION: SEQ ID NO: 22:</p> <p>US-09-490-153-22</p>								
<p>Query Match 78.8%; Score 524.5; DB 2; Length 117;</p> <p>Best Local Similarity 81.7%; Pred. No. 7.5e-45;</p> <p>Matches 103; Conservative 5; Mismatches 9; Indels 9; Gaps 1;</p>								

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Qy 61 AQKFGQVMTTRNTSISTAYMELSLRSEDPAVYVCARDVMTTGGVIVHYGMDVWGQGT 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 AQKFGQVMTTRNTSISTAYMELSLRSDPAVYVCARDVMTTGGVIVHYGMDVWGQGT 111
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 121 TTVSS 126
| | | | |
Db 112 LTVSS 117
| | | | |

RESULT 13
US-08-545-809A-96
; Sequence 96, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasaku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-96

Query Match 77.6%; Score 517; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-44;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWPNPNSGNTGY 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 20 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWPNPNSGNTGY 79
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 AQKFGQVMTTRNTSISTAYMELSLRSEDPAVYVCAR 98
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 80 AQKFGQVMTTRNTSISTAYMELSLRSEDPAVYVCAR 117
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 14
US-09-515-697-96
; Sequence 96, Application US/09515697
; Patent No. 6936705
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasaku
; APPLICANT: Matsuda, Fumihiko
```

```
;
;
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,697
; FILING DATE: 29-Feb-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809
; FILING DATE: 27-MAR-1996
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-09-515-697-96

Query Match 77.6%; Score 517; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-44;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWPNPNSGNTGY 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 20 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWPNPNSGNTGY 79
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 AQKFGQVMTTRNTSISTAYMELSLRSEDPAVYVCAR 98
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 80 AQKFGQVMTTRNTSISTAYMELSLRSEDPAVYVCAR 117
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 15
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match      76.5%; Score 509.5; DB 2; Length 470;
Best Local Similarity 78.6%; Pred. No. 1.1e-42;
Matches 99; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMPNSGNTGY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMPNSGNTGY 60
QY 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSDDTAVYYCARTYYDDSG-YHDAFDINGQGT 120
Db 80 AQKFGQGRVTMTTRDTSISTAYMELSLRSDDTAVYYCARTYYDDSG-YHDAFDINGQGT 120
QY 121 TVTVSS 126
Db 139 MTVVSS 144

Search completed: April 25, 2007, 04:08:32
Job time : 15.839 secs
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Result No.	Query			ID	Description
	Score	Match	Length		
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2	666	100.0	126	4	US-10-041-860-199
3	666	100.0	126	4	US-10-041-860-236
4	666	100.0	126	4	US-10-041-860-294
5	666	100.0	126	4	US-10-665-383-22
6	605	90.8	126	4	US-10-041-860-40
7	605	90.8	126	4	US-10-041-860-204
8	605	90.8	126	4	US-10-041-860-241
9	605	90.8	126	4	US-10-041-860-349
10	605	90.8	126	4	US-10-665-383-58
11	604	90.7	126	4	US-10-041-860-19
12	604	90.7	126	4	US-10-041-860-201
13	604	90.7	126	4	US-10-041-860-288
14	604	90.7	126	4	US-10-665-383-18
15	600	90.1	126	4	US-10-041-860-37
16	600	90.1	126	4	US-10-041-860-202
17	600	90.1	126	4	US-10-041-860-239
18	600	90.1	126	4	US-10-665-383-74
19	593.5	89.1	125	4	US-10-041-860-38
20	593.5	89.1	125	4	US-10-041-860-203
21	593.5	89.1	125	4	US-10-041-860-240
22	593.5	89.1	125	4	US-10-041-860-343
23	593.5	89.1	125	4	US-10-665-383-54
24	593	89.0	122	4	US-10-269-805-61
25	593	89.0	122	5	US-10-982-440-61
26	590	88.6	125	4	US-10-041-860-238
27	580.5	87.2	127	4	US-10-041-860-44

```
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-199

Query Match      100.0%; Score 666; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTNTSISTAYMELSLRSEDATVYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSLRSEDATVYCARDVMTFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 3
US-10-041-860-236
; Sequence 236, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-236

Query Match      100.0%; Score 666; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTNTSISTAYMELSLRSEDATVYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSLRSEDATVYCARDVMTFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126
```

```
Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 4
US-10-041-860-294
; Sequence 294, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 294
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-294

Query Match      100.0%; Score 666; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTNTSISTAYMELSLRSEDATVYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSLRSEDATVYCARDVMTFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 5
US-10-665-383-22
; Sequence 22, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: Laroche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2003-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-22
```

Query Match 100.0%; Score 666; DB 4; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-56;  
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60  
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTFGGVIHYGMDVWGQGT 120  
 Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTFGGVIHYGMDVWGQGT 120

Qy 121 TTVTVSS 126  
 Db 121 TTVTVSS 126

RESULT 6  
 US-10-041-860-40  
 ; Sequence 40, Application US/10041860  
 ; Publication No. US20030157109A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Corvalan, Jose R.F.  
 ; APPLICANT: Jia, Xiao-Chi  
 ; APPLICANT: Feng, Xiao  
 ; APPLICANT: Yang, Xiao-Dong  
 ; APPLICANT: Chen, Francine  
 ; APPLICANT: Gazit, Gadi  
 ; APPLICANT: Weber, Richard  
 ; APPLICANT: Bezabeh, Binyam  
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
 ; FILE REFERENCE: ABGENIX.051A  
 ; CURRENT APPLICATION NUMBER: US/10/041.860  
 ; CURRENT FILING DATE: 2002-01-07  
 ; NUMBER OF SEQ ID NOS: 377  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 40  
 ; LENGTH: 126  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-041-860-40

Query Match 90.8%; Score 605; DB 4; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 6.5e-50;  
 Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60  
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTFGGVIHYGMDVWGQGT 120  
 Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTFGGVIHYGMDVWGQGT 120

Qy 121 TTVTVSS 126  
 Db 121 TTVTVSS 126

RESULT 7  
 US-10-041-860-204  
 ; Sequence 204, Application US/10041860  
 ; Publication No. US20030157109A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Corvalan, Jose R.F.  
 ; APPLICANT: Jia, Xiao-Chi  
 ; APPLICANT: Feng, Xiao  
 ; APPLICANT: Yang, Xiao-Dong  
 ; APPLICANT: Chen, Francine  
 ; APPLICANT: Gazit, Gadi  
 ; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam  
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
 ; FILE REFERENCE: ABGENIX.051A  
 ; CURRENT APPLICATION NUMBER: US/10/041.860  
 ; CURRENT FILING DATE: 2002-01-07  
 ; NUMBER OF SEQ ID NOS: 377  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 204  
 ; LENGTH: 126  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-041-860-204

Query Match 90.8%; Score 605; DB 4; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 6.5e-50;  
 Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60  
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTFGGVIHYGMDVWGQGT 120  
 Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTFGGVIHYGMDVWGQGT 120

Qy 121 TTVTVSS 126  
 Db 121 TTVTVSS 126

RESULT 8  
 US-10-041-860-241  
 ; Sequence 241, Application US/10041860  
 ; Publication No. US20030157109A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Corvalan, Jose R.F.  
 ; APPLICANT: Jia, Xiao-Chi  
 ; APPLICANT: Feng, Xiao  
 ; APPLICANT: Yang, Xiao-Dong  
 ; APPLICANT: Chen, Francine  
 ; APPLICANT: Gazit, Gadi  
 ; APPLICANT: Weber, Richard  
 ; APPLICANT: Bezabeh, Binyam  
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
 ; FILE REFERENCE: ABGENIX.051A  
 ; CURRENT APPLICATION NUMBER: US/10/041.860  
 ; CURRENT FILING DATE: 2002-01-07  
 ; NUMBER OF SEQ ID NOS: 377  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 241  
 ; LENGTH: 126  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-041-860-241

Query Match 90.8%; Score 605; DB 4; Length 126;  
 Best Local Similarity 89.7%; Pred. No. 6.5e-50;  
 Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60  
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTFGGVIHYGMDVWGQGT 120  
 Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTFGGVIHYGMDVWGQGT 120

Qy 121 TTVTVSS 126  
 Db 121 TTVTVSS 126

```
RESULT 9
US-10-041-860-349
; Sequence 349, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 349
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-349

Query Match          90.8%; Score 605; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 6.5e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYDINNVROATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYDINNVROATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSSLSRSEDATVYVCARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSSLSRSEDATVYVCARDVMTITFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 11
US-10-041-860-19
; Sequence 19, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-19

Query Match          90.7%; Score 604; DB 4; Length 126;
Best Local Similarity 91.3%; Pred. No. 8.1e-50;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYDINNVROATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYDINNVROATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSSLSRSEDATVYVCARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSSLSRSEDATVYVCARDVMTITFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 12
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYDINNVROATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYDINNVROATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSSLSRSEDATVYVCARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSSLSRSEDATVYVCAREGIAVAGTYYYYYGGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

Query Match          90.8%; Score 605; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 6.5e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYDINNVROATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYDINNVROATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSSLSRSEDATVYVCARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSSLSRSEDATVYVCARDIVVVVTTATDYIYGGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 10
US-10-665-383-58
; Sequence 58, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGFD-ANTIBODIES
; FILE REFERENCE: AGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665.383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-58

Query Match          90.8%; Score 605; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 6.5e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYDINNVROATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYDINNVROATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSSLSRSEDATVYVCARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSSLSRSEDATVYVCARDIVVVVTTATDYIYGGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126
```

```
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

Query Match          90.7%; Score 604; DB 4; Length 126;
Best Local Similarity 91.3%; Pred. No. 8.1e-50;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYVCARDVMITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYVCAREGIAVAGTYYYYYGMVDVWGQGT 120

Qy 121 TTVVSS 126
Db 121 TTVVSS 126

RESULT 13
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao-Dong
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288

Query Match          90.7%; Score 604; DB 4; Length 126;
Best Local Similarity 91.3%; Pred. No. 8.1e-50;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYVCARDVMITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYVCAREGIAVAGTYYYYYGMVDVWGQGT 120

Qy 121 TTVVSS 126
Db 121 TTVVSS 126

RESULT 14
US-10-665-383-18
; Sequence 18, Application US/10665383
; Publication No. US20040141969A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichtenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-18

Query Match          90.7%; Score 604; DB 4; Length 126;
Best Local Similarity 91.3%; Pred. No. 8.1e-50;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYVCARDVMITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYVCAREGIAVAGTYYYYYGMVDVWGQGT 120

Qy 121 TTVVSS 126
Db 121 TTVVSS 126

RESULT 15
US-10-041-860-37
; Sequence 37, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-37

Query Match          90.1%; Score 600; DB 4; Length 126;
Best Local Similarity 88.9%; Pred. No. 1.9e-49;
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYVCARDVMITFGGVIVHYGMDVWGQGT 120
```



Db 61 AOKFOGRVTMTNTSLSTAYMELSLRSEDVAVYCARDIVVVVAATNYNGMDVNGQGT 120  
Qy 121 TTVVSS 126  
Db 121 TTVVSS 126

Search completed: April 25, 2007, 04:22:51  
Job time : 47.6271 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:23:02 ; Search time 49 Seconds  
(without alignments)  
533.620 Million cell updates/sec

Title: US-10-665-383-22

Perfect score: 666

Sequence: 1 QVQLVQSGAEVKPKGASVKV.....VIVHGMVDVWGQGTTVTVSS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 947558 seqs, 205760075 residues

Total number of hits satisfying chosen parameters: 947558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB pep.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	666	100.0	126	7	US-11-109-181-21
2	666	100.0	126	7	US-11-109-181-199
3	666	100.0	126	7	US-11-109-181-236
4	666	100.0	126	7	US-11-109-181-294
5	605	90.8	126	7	US-11-109-181-40
6	605	90.8	126	7	US-11-109-181-204
7	605	90.8	126	7	US-11-109-181-241
8	605	90.8	126	7	US-11-109-181-349
9	604	90.7	126	7	US-11-109-181-19
10	604	90.7	126	7	US-11-109-181-201
11	604	90.7	126	7	US-11-109-181-288
12	600	90.1	126	7	US-11-109-181-37
13	600	90.1	126	7	US-11-109-181-202
14	600	90.1	126	7	US-11-109-181-239
15	593.5	89.1	125	7	US-11-109-181-38
16	593.5	89.1	125	7	US-11-109-181-203
17	593.5	89.1	125	7	US-11-109-181-240
18	593.5	89.1	125	7	US-11-109-181-343
19	591.5	88.8	126	7	US-11-433-924-94
20	590	88.6	125	7	US-11-109-181-238
21	585	87.8	122	7	US-11-433-924-254
22	580.5	87.2	127	7	US-11-109-181-44
23	580.5	87.2	127	7	US-11-109-181-205
24	580.5	87.2	127	7	US-11-109-181-242
25	580.5	87.2	127	7	US-11-109-181-360

26	567.5	85.2	125	7	US-11-109-181-48	Sequence 48, Appl
27	567.5	85.2	125	7	US-11-109-181-200	Sequence 200, App
28	567.5	85.2	125	7	US-11-109-181-237	Sequence 237, App
29	567.5	85.2	125	7	US-11-109-181-372	Sequence 372, App
30	554	83.2	450	7	US-11-396-178-20	Sequence 20, Appl
31	553.5	83.1	199	5	US-09-784-950-29	Sequence 29, Appl
32	553.5	83.1	199	7	US-11-366-003-29	Sequence 29, Appl
33	553	83.0	116	7	US-11-433-924-14	Sequence 14, Appl
34	546.5	82.1	257	7	US-11-327-917-15	Sequence 15, Appl
35	539.5	81.0	123	7	US-11-410-886-69	Sequence 69, Appl
36	539.5	81.0	449	7	US-11-410-886-22	Sequence 22, Appl
37	536.5	80.6	123	7	US-11-410-886-49	Sequence 49, Appl
38	536.5	80.6	126	7	US-11-311-939-425	Sequence 425, App
39	536.5	80.6	126	7	US-11-311-939-429	Sequence 429, App
40	536.5	80.6	449	7	US-11-410-886-6	Sequence 6, Appl
41	533.5	80.1	203	5	US-09-784-950-27	Sequence 27, Appl
42	533.5	80.1	203	7	US-11-366-003-27	Sequence 27, Appl
43	529	79.4	121	7	US-11-311-939-586	Sequence 586, App
44	526	79.0	120	7	US-11-304-986-22	Sequence 22, Appl
45	526	79.0	120	7	US-11-303-478-46	Sequence 46, Appl

#### ALIGNMENTS

#### RESULT 1

US-11-109-181-21  
; Sequence 21, Application US/11109181  
; Publication No. US20060293506A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; TITLE OF INVENTION: THEROFO  
; FILE REFERENCE: AGENIX.051A  
; CURRENT APPLICATION NUMBER: US/11/109,181  
; CURRENT FILING DATE: 2005-04-18  
; PRIOR APPLICATION NUMBER: US/10/041,860  
; PRIOR FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-11-109-181-21

Query Match 100.0%; Score 666; DB 7; Length 126;  
Best Local Similarity 100.0%; Pred. No. 1.8e-56;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINNVROATQGLEWGMGNPNSGNTGY 60  
Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINNVROATQGLEWGMGNPNSGNTGY 60  
QY 61 AQKFGQRTVMTNTSISTAYMELSLRSRSDTAVYICARDVMTFGGVIVHYGMDVWGQGT 120  
Db 61 AQKFGQRTVMTNTSISTAYMELSLRSRSDTAVYICARDVMTFGGVIVHYGMDVWGQGT 120  
QY 121 TVTVSS 126  
Db 121 TVTVSS 126

#### RESULT 2

US-11-109-181-199  
; Sequence 199, Application US/11109181

```
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-199

Query Match      100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 4
US-11-109-181-294
; Sequence 294, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 294
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-294

Query Match      100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 5
US-11-109-181-40
; Sequence 40, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-236

Query Match      100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 3
US-11-109-181-236
; Sequence 236, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-236

Query Match      100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-204

Query Match          90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60
Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 6
US-11-109-181-204
; Sequence 204, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-241

Query Match          90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60
Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 7
US-11-109-181-241
; Sequence 241, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-241

Query Match          90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60
Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 8
US-11-109-181-349
; Sequence 349, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 349
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-204

Query Match          90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60
Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126
```

```
; ORGANISM: homo sapiens
US-11-109-181-349

Query Match          90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.6e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AQKQFGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFTGGVIVHYGMDVWGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKQFGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFTGGVIVHYGMDVWGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TTVTVSS 126
    |||||
Db 121 TTVTVSS 126
    |||||

RESULT 9
US-11-109-181-19
; Sequence 19, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-19

Query Match          90.7%; Score 604; DB 7; Length 126;
Best Local Similarity 91.3%; Pred. No. 1.6e-50;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AQKQFGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFTGGVIVHYGMDVWGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKQFGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFTGGVIVHYGMDVWGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TTVTVSS 126
    |||||
Db 121 TTVTVSS 126
    |||||

RESULT 10
US-11-109-181-201
; Sequence 201, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
```

```
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-201

Query Match          90.7%; Score 604; DB 7; Length 126;
Best Local Similarity 91.3%; Pred. No. 1.6e-50;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AQKQFGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFTGGVIVHYGMDVWGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKQFGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFTGGVIVHYGMDVWGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TTVTVSS 126
    |||||
Db 121 TTVTVSS 126
    |||||

RESULT 11
US-11-109-181-288
; Sequence 288, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-288

Query Match          90.7%; Score 604; DB 7; Length 126;
Best Local Similarity 91.3%; Pred. No. 1.6e-50;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AQKQFGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFTGGVIVHYGMDVWGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKQFGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMTFTGGVIVHYGMDVWGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TTVTVSS 126
    |||||
Db 121 TTVTVSS 126
    |||||
```

```

QY 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126

RESULT 12
US-11-109-181-37
; Sequence 37, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-37

Query Match 90.1%; Score 600; DB 7; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.8e-50;
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATGQGLEWMGMNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATGQGLEWMGMNPNPNSGNTGY 60
QY 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126

RESULT 13
US-11-109-181-202
; Sequence 202, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-202

Query Match 90.1%; Score 600; DB 7; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.8e-50;
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATGQGLEWMGMNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATGQGLEWMGMNPNPNSGNTGY 60
QY 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126

RESULT 14
US-11-109-181-239
; Sequence 239, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 239
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-239

Query Match 90.1%; Score 600; DB 7; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.8e-50;
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATGQGLEWMGMNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATGQGLEWMGMNPNPNSGNTGY 60
QY 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126

RESULT 15
US-11-109-181-38

```

```

; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-202

Query Match 90.1%; Score 600; DB 7; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.8e-50;
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATGQGLEWMGMNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATGQGLEWMGMNPNPNSGNTGY 60
QY 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126

RESULT 14
US-11-109-181-239
; Sequence 239, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 239
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-239

Query Match 90.1%; Score 600; DB 7; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.8e-50;
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATGQGLEWMGMNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATGQGLEWMGMNPNPNSGNTGY 60
QY 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFOGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126

RESULT 15
US-11-109-181-38

```

```

; Sequence 38, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-38

Query Match      89.1%; Score 593.5; DB 7; Length 125;
Best Local Similarity 91.3%; Pred. No. 1.6e-49;
Matches 115; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

Qy      1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
Db      1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60

Qy      61 AQKFQGRVTMTNTSISTAYMELSSLRSEDATVYICARDVMITFGGVIVHYGMDVMCGGT 120
Db      61 AQKFQGRVTMTNTSISTAYMELSSLRSEDATVYICARGSGSY-GYDYIYGGMDVMCGGT 119

Qy      121 TTVTVSS 126
Db      120 TTVTVSS 125

```

Search completed: April 25, 2007, 04:27:44  
Job time : 49.5847 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 93 Seconds  
(without alignments)  
564.248 Million cell updates/sec

Title: US-10-665-383-24  
Perfect score: 558  
Sequence: 1 DIQWTSFSLASVGRVT.....CLOHNSDPCSFQGTGLEIR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

A Genesep\_200701:\*

- 1: Genesep1980s:\*
- 2: Genesep1990s:\*
- 3: Genesep2000s:\*
- 4: Genesep2001s:\*
- 5: Genesep2002s:\*
- 6: Genesep2003as:\*
- 7: Genesep2003bs:\*
- 8: Genesep2004s:\*
- 9: Genesep2005s:\*
- 10: Genesep2006s:\*
- 11: Genesep2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	107	7	Adk18598 Anti-huma
2	558	100.0	107	7	Adk18838 Anti-huma
3	558	100.0	107	7	Adk18837 Anti-huma
4	558	100.0	107	7	Adk18873 Anti-huma
5	558	100.0	107	7	Adk18803 Anti-huma
6	558	100.0	107	8	Adl25414 Human mAb
7	542	97.1	107	8	AdS84414 Human ant
8	542	97.1	107	8	Adr68556 Anti-EPO-
9	542	97.1	234	8	AdS84470 Human ant
10	542	97.1	234	8	Adr68612 Human ant
11	539	96.6	107	8	AdS84402 Human ant
12	539	96.6	107	8	Adr68544 Anti-EPO-
13	539	96.6	234	8	AdS84452 Human ant
14	539	96.6	234	8	Adr68594 Human ant
15	528	94.6	107	7	Adk18841 Anti-huma
16	528	94.6	108	10	Aej60732 Sulfoore
17	528	94.6	236	5	ABG77160 Germline
18	528	94.6	236	8	ADR28582 Human ant
19	528	94.6	236	10	Aef54367 Human lig
20	528	94.6	236	10	Aef54346 Human lig
21	528	94.6	236	10	Aef34918 Human ger
22	528	94.6	236	10	Ael09667 Anti-IGF1

#### ALIGNMENTS

#### RESULT 1

ADK18598  
ID ADK18598 standard; protein; 107 AA.

XX AC ADK18598;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-human PDGF-D antibody light chain protein sequence.

XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX OS Homo sapiens.

XX PN WO2003057857-A2.

XX PD 17-JUL-2003.

XX PF 06-JAN-2003; 2003WO-US000398.

XX PR 07-JAN-2002; 2002US-00041860.

XX PA (ABGE-) ABGENIX INC.

XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R; Bezabeh B;

XX DR WPI; 2003-587119/55.

XX PT New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

XX PS Disclosure; SEQ ID NO 22; 255pp; English.

XX CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

23	528	94.6	236	10	ABL59900	Ael59900 Light cha
24	527	94.4	107	5	ABG30494	Abg30494 Human ant
25	527	94.4	108	8	ADS16571	Ads16571 Human ant
26	525	94.1	107	7	ADC99789	Adc99789 Anti-huma
27	525	94.1	107	7	ADD05393	Adg05393 Anti-MUC1
28	525	94.1	107	7	ADF09831	Adf09831 Human ant
29	525	94.1	107	7	ADK18842	Adk18842 Anti-huma
30	525	94.1	107	7	ADK18916	Adk18916 Anti-huma
31	525	94.1	107	7	ADK18892	Adk18892 Anti-huma
32	525	94.1	107	7	ADK18612	Adk18612 Anti-huma
33	525	94.1	107	7	ADK18602	Adk18602 Anti-huma
34	525	94.1	107	7	ADK18810	Adk18810 Anti-huma
35	525	94.1	107	7	ADK18844	Adk18844 Anti-huma
36	525	94.1	107	7	ADK18808	Adk18808 Anti-huma
37	525	94.1	107	7	ADK18807	Adk18807 Anti-huma
38	525	94.1	107	7	ADK18604	Adk18604 Murine-ex
39	525	94.1	107	7	ADP03996	Adp03996 Human mAb
40	525	94.1	107	8	ADL25422	Adl25422 Human mAb
41	525	94.1	107	8	ADL25426	Adl25426 Human mAb
42	525	94.1	107	8	ADL25442	Adl25442 Human mAb
43	525	94.1	107	8	ADO07289	Ado07289 Human pro
44	525	94.1	107	8	ADP22368	Adp22368 Human ant
45	525	94.1	107	8	ADP22401	Adp22401 Human ant





DE Anti-human PDGF-D antibody protein related sequence #99.

KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX Homo sapiens.

XX WO2003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth  
factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.

XX Disclosure; SEQ ID NO 297; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to  
platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
treating chronic and recurrent human diseases, such as inflammation,  
autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
useful for modulating collagen formation, and for staging various  
cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
generated using an active protein fragment of the gene product from the  
clone 30664188.0.99 arising in the conditioned medium obtained when  
HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
sequence corresponds to a protein used in the invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 558; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2e-34;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDTLTITSLQPEDFATYICLQHNSDPCSFQGTGKLEIR 107  
Db 61 RFGSGSGTDTLTITSLQPEDFATYICLQHNSDPCSFQGTGKLEIR 107

RESULT 5

ADK18803

ID ADK18803 standard; protein; 107 AA.

XX ADK18803;

XX 06-MAY-2004 (first entry)

XX Anti-human PDGF-D antibody protein related sequence #29.

XX antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX Homo sapiens.

XX WO2003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX

PR 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth  
factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.

XX Disclosure; SEQ ID NO 227; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to  
platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
treating chronic and recurrent human diseases, such as inflammation,  
autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
useful for modulating collagen formation, and for staging various  
cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
generated using an active protein fragment of the gene product from the  
clone 30664188.0.99 arising in the conditioned medium obtained when  
HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
sequence corresponds to a protein used in the invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 558; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2e-34;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDTLTITSLQPEDFATYICLQHNSDPCSFQGTGKLEIR 107

Db 61 RFGSGSGTDTLTITSLQPEDFATYICLQHNSDPCSFQGTGKLEIR 107

RESULT 6

ADL25414

ID ADL25414 standard; protein; 107 AA.

XX ADL25414;

XX 17-JUN-2004 (first entry)

XX Human mAb 1.19 light chain variable region protein SEQ ID NO:24.

XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;  
nephritis; mesangial cell proliferation inhibition;  
mesangial proliferative glomerulonephritis; nephrotropic;  
antiinflammatory; dermatological; immunosuppressive; antidiabetic;  
gene therapy; human; monoclonal antibody; mAb.

XX Homo sapiens.

XX WO2004024098-A2.

XX 25-MAR-2004.

XX 16-SEP-2003; 2003WO-US029414.

XX 16-SEP-2002; 2002US-0411137P.

XX (ABGE-) ABGENIX INC.

XX (CURA-) CURAGEN CORP.

XX Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;

XX WPI; 2004-269881/25.

DR N-PSDB; ADL25413.  
XX Use of an antibody or its binding fragment that binds platelet derived  
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating  
PT nephritis.  
XX  
XX Disclosure; SEQ ID NO 24; 115pp; English.  
XX  
XX The present invention describes an antibody or its binding fragment that  
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is  
CC useful in preparing a medicament for treating nephritis. Also described:  
CC (1) a method of detecting nephritis; (2) a method of treating nephritis;  
CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method  
CC of treating mesangial proliferative glomerulonephritis. The antibody has  
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and  
CC antidiabetic activities, and can be used in gene therapy. The antibody or  
CC its binding fragment, that binds PDGF-DD, can be used in preparing a  
CC medicament for treating nephritis and related disorders, e.g., mesangial  
CC proliferative glomerulonephritis. The present sequence represents a human  
CC monoclonal antibody (mAb) variable region sequence, which is used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 107 AA;  
XX  
XX Query Match 100.0%; Score 558; DB 8; Length 107;  
XX Best Local Similarity 100.0%; Pred. No. 2e-34;  
XX Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 DIQWTQSPSSLSASVGDRTVITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60  
XX  
XX 1 DIQWTQSPSSLSASVGDRTVITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60  
XX  
XX 61 RFSGSGGTDTFTLTISLQPEDFATYTCLOHNSDPCSFQGTKEIR 107  
XX  
XX 61 RFSGSGGTDTFTLTISLQPEDFATYTCLOHNSDPCSFQGTKEIR 107  
XX  
XX  
XX RESULT 7  
XX ADS84414  
XX ID ADS84414 standard; protein; 107 AA.  
XX AC ADS84414;  
XX  
XX DT 18-NOV-2004 (first entry)  
XX  
XX DE Human anti-EPO-R antibody light chain variable region SEQ ID NO:53.  
XX  
XX human; erythropoietin receptor; EPO receptor;  
XX erythropoietin receptor binding antibody; EPO receptor binding antibody;  
XX antianaemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;  
XX wound healing; neural cell damage protection;  
XX neural tissue damage protection; brain injury; spinal cord injury;  
XX stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.  
XX  
XX OS Homo sapiens.  
XX  
XX WO2004035603-A2.  
XX  
XX 29-APR-2004.  
XX  
XX 14-OCT-2003; 2003WO-US032243.  
XX  
XX 14-OCT-2002; 2002US-00269711.  
XX  
XX 10-OCT-2003; 2003US-00684109.  
XX  
XX (ABBO ) ABBOTT LAB.  
XX  
XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
XX WPI; 2004-348433/32.  
XX N-PSDB; ADS84413.  
XX  
XX New antibodies that bind to or activate an endogenous human

PT erythropoietin receptor, useful for diagnosing, preventing or treating  
PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
XX anemia.  
XX Claim 10; SEQ ID NO 53; 192pp; English.  
XX  
XX The present invention describes an antibody or its fragment that binds to  
CC or activates an endogenous activity of a human erythropoietin (EPO)  
CC receptor in a mammal, but does not interact with a peptide having a  
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
CC methods of modulating or activating an endogenous activity of a human EPO  
CC receptor in a mammal, comprising administering to the mammal a  
CC therapeutic amount of the above antibody or its fragment to modulate or  
CC activate the receptor; (2) a method of treating a mammal suffering from  
CC aplasia, comprising administering to the mammal a therapeutic amount of  
CC the above antibody or its fragment to modulate or activate the receptor;  
CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
CC an isolated and purified polynucleotide sequence, and their fragments,  
CC complements and degenerate codon equivalents; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antianaemic, neuroprotective and vulnary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from  
CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence represents a human anti-EPO-R antibody light  
CC chain variable region, which is given in the exemplification of the  
XX present invention.  
XX  
XX Sequence 107 AA;  
XX  
XX Query Match 97.1%; Score 542; DB 8; Length 107;  
XX Best Local Similarity 97.2%; Pred. No. 3.1e-33;  
XX Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 DIQWTQSPSSLSASVGDRTVITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60  
XX  
XX 1 DIQWTQSPSSLSASVGDRTVITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQSGVPS 60  
XX  
XX 61 RFSGSGGTDTFTLTISLQPEDFATYTCLOHNSDPCSFQGTKEIR 107  
XX  
XX 61 RFSGSGGTDTFTLTISLQPEDFATYTCLOHNSDPCSFQGTKEIR 107  
XX  
XX  
XX RESULT 8  
XX ADR68556  
XX ID ADR68556 standard; protein; 107 AA.  
XX AC ADR68556;  
XX  
XX DT 02-DEC-2004 (first entry)  
XX  
XX DE Anti-EPO-R-antibody light chain variable region seqid 53.  
XX  
XX antianaemic; respiratory; vulnary; gene therapy; vaccine;  
XX erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
XX hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
XX wound healing; neural cell damage; tissue damage; brain injury;  
XX spinal cord injury; stroke; anti-EPO-R-antibody; light chain;  
XX variable region.  
XX  
XX OS Homo sapiens.  
XX  
XX US2004175379-A1.  
XX  
XX 09-SEP-2004.  
XX  
XX 10-OCT-2003; 2003US-00684109.  
XX

PR 14-OCT-2002; 2002US-0418031P.  
 XX (DEVIR) DEVRIES P J.  
 PA (OSTR) OSTROW D H.  
 PA (REIL) REILLY E B.  
 PA (GREG) GREEN L L.  
 PA (WIEL) WIELER J.  
 XX  
 PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
 XX WPI: 2004-661369/64.  
 DR N-PSDB; ADR68555.  
 XX  
 XX New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.  
 XX  
 XX Claim 10; SEQ ID NO 53; 156pp; English.  
 XX  
 XX The invention describes an antibody or its fragment that activates an  
 CC endogenous activity or capable of binding to a human erythropoietin  
 CC receptor in a mammal, or that comprises at least one heavy or light chain  
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 CC given in the specification. Also described are: a method of activating or  
 CC modulating an endogenous activity of a human erythropoietin receptor in a  
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
 CC isolated and purified polynucleotide sequence selected from 28 sequences  
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
 CC the specification, and their fragments, complements, and degenerate codon  
 CC equivalents; and an isolated and purified amino acid sequence selected  
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 CC their fragments. The antibody or its antibody fragment that activates or  
 CC modulates the activity of the receptor is useful in a method of treating  
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
 CC treating disorders characterised by decreased or subnormal levels of  
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 CC reduced blood flow. They are also useful for promoting wound healing or  
 CC for protecting against neural cell and/or tissue damage, resulting from  
 CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 CC useful for identifying or diagnosing mammals having dysfunctional  
 CC erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R  
 CC -antibody light chain variable region.  
 XX  
 XX Sequence 107 AA;  
 SQ  
 Query Match 97.1%; Score 542; DB 8; Length 107;  
 Best Local Similarity 97.2%; Pred. No. 3.1e-33;  
 Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLWGYYQKPKAPKRLIYAASLSQSGVPS 60  
 Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLWGYYQKPKAPKRLIYAASLSQSGVPS 60  
 QY 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107  
 Db 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107  
 RESULT 9  
 ID ADS84470  
 XX ADS84470 standard; protein; 234 AA.  
 AC ADS84470;  
 XX  
 XX 18-NOV-2004 (first entry)  
 DT  
 XX Human anti-EPO-R antibody Ab467 light chain SEQ ID NO:109.  
 DE  
 XX

human; erythropoietin receptor; EPO receptor;  
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 KW antianaemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;  
 KW wound healing; neural cell damage protection;  
 KW neural tissue damage protection; brain injury; spinal cord injury;  
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004035603-A2.  
 XX  
 PD 29-APR-2004.  
 XX  
 PF 14-OCT-2003; 2003WO-US032243.  
 XX  
 PR 14-OCT-2002; 2002US-00269711.  
 PR 10-OCT-2003; 2003US-00684109.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
 XX  
 DR WPI: 2004-348433/32.  
 DR N-PSDB; ADS84468, ADS84469.  
 XX  
 XX New antibodies that bind to or activate an endogenous human  
 PT erythropoietin receptor, useful for diagnosing, preventing or treating  
 PT disorders associated with dysfunctional erythropoietin receptor; e.g.  
 PT anemia.  
 XX  
 XX Disclosure; SEQ ID NO 109; 192pp; English.  
 CC  
 CC The present invention describes an antibody or its fragment that binds to  
 CC or activates an endogenous activity of a human erythropoietin (EPO)  
 CC receptor in a mammal, but does not interact with a peptide having a  
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 CC methods of modulating or activating an endogenous activity of a human EPO  
 CC receptor in a mammal, comprising administering to the mammal a  
 CC therapeutic amount of the above antibody or its fragment to modulate or  
 CC activate the receptor; (2) a method of treating a mammal suffering from  
 CC aplasia, comprising administering to the mammal a therapeutic amount of  
 CC the above antibody or its fragment to modulate or activate the receptor;  
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 CC an isolated and purified polynucleotide sequence, and their fragments;  
 CC complements and degenerate codon equivalents; and (5) an isolated and  
 CC purified amino acid sequence, and their fragments. The EPO receptor  
 CC binding antibody has antianaemic, neuroprotective and vulnary  
 CC activities, and can be used in gene therapy. The compositions and methods  
 CC from the present invention can be used for modulating an endogenous  
 CC activity of a human EPO receptor or for treating mammals suffering from  
 CC aplasia or anaemia. They may also be used for identifying mammals having  
 CC a dysfunctional EPO receptor. The composition may also be used in  
 CC promoting wound healing or in protecting against neural cell and/or  
 CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 CC like. The present sequence represents a human anti-EPO-R antibody light  
 CC chain, which is given in the exemplification of the present invention.  
 XX  
 XX Sequence 234 AA;  
 SQ  
 Query Match 97.1%; Score 542; DB 8; Length 234;  
 Best Local Similarity 97.2%; Pred. No. 6.4e-33;  
 Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLWGYYQKPKAPKRLIYAASLSQSGVPS 60  
 Db 21 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLWGYYQKPKAPKRLIYAASLSQSGVPS 80  
 QY 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107  
 Db 81 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGGTKLEIR 127

RESULT 10  
ADR68612  
ID ADR68612 standard; protein; 234 AA.  
XX  
AC ADR68612;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human antibody Ab467 light chain polypeptide seqid 109.  
XX  
DE antianemic; respiratory; vulnerary; gene therapy; vaccine;  
KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
KW wound healing; neural cell damage; tissue damage; brain injury;  
KW spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;  
KW Ab467.  
XX  
OS Homo sapiens.  
XX  
PN US2004175379-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 10-OCT-2003; 2003US-00684109.  
XX  
PR 14-OCT-2002; 2002US-0418031P.  
XX  
PA (DEVRIE/) DEVRIES P J.  
PA (OSTROW/) OSTROW D H.  
PA (REILLY/) REILLY E B.  
PA (GREEN/) GREEN L L.  
PA (WIELER/) WIELER J.  
XX  
PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
XX  
XX WPI; 2004-661369/64.  
DR N-PSDB; ADR68610.  
XX  
XX New antibody or its antibody fragment that activates an endogenous  
PT activity or is capable of binding to a human erythropoietin receptor in a  
PT mammal, useful for treating a mammal suffering aplasia or anaemia.  
XX  
PS Disclosure; SEQ ID NO 109; 156pp; English.  
XX  
XX The invention describes an antibody or its fragment that activates an  
CC endogenous activity or capable of binding to a human erythropoietin  
CC receptor in a mammal, or that comprises at least one heavy or light chain  
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
CC given in the specification. Also described are: a method of activating or  
CC modulating an endogenous activity of a human erythropoietin receptor in a  
CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
CC isolated and purified polynucleotide sequence selected from 28 sequences  
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
CC the specification, and their fragments, complements, and degenerate codon  
CC equivalents; and an isolated and purified amino acid sequence selected  
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
CC their fragments. The antibody or its antibody fragment that activates or  
CC modulates the activity of the receptor is useful in a method of treating  
CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
CC treating disorders characterised by decreased or subnormal levels of  
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
CC hypoxia and/or diseases characterised by inadequate blood circulation or  
CC reduced blood flow. They are also useful for promoting wound healing or  
CC for protecting against neural cell and/or tissue damage, resulting from  
CC brain/spinal cord injury, stroke and the like. The antibodies are also  
CC useful for identifying or diagnosing mammals having dysfunctional  
CC erythropoietin receptor. This sequence represents a human Ab467 antibody  
CC light chain polypeptide.  
XX

SO Sequence 234 AA;  
Query Match 97.1%; Score 542; DB 8; Length 234;  
Best Local Similarity 97.2%; Pred. No. 6.4e-33;  
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 DIQWTQSPSSLSASVGRVITTCRASQGIKNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60  
Db 21 DIQWTQSPSSLSASVGRVITTCRASQGIKNDLQWYQKPGKAPKRLIYAASSLSQGVPS 80  
Qy 61 RFSGSGSGTFTLTSSIQPEDFAFYCYCLOHNSDPCSPFGQGTKEIR 107  
Db 81 RFSGSGSGTFTLTSSIQPEDFAFYCYCLOHNSDPCSPFGQGTKEIR 127  
RESULT 11  
ADS84402  
ID ADS84402 standard; protein; 107 AA.  
XX  
AC ADS84402;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human anti-EPO-R antibody light chain variable region SEQ ID NO:41.  
XX  
KW human; erythropoietin receptor; EPO receptor;  
KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
KW antianemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
KW wound healing; neural cell damage protection;  
KW neural tissue damage protection; brain injury; spinal cord injury;  
KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035603-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 14-OCT-2003; 2003WO-US032243.  
XX  
PR 14-OCT-2002; 2002US-00269711.  
PR 10-OCT-2003; 2003US-00684109.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
XX  
XX WPI; 2004-348433/32.  
DR N-PSDB; ADS84401.  
XX  
PT New antibodies that bind to or activate an endogenous human  
PT erythropoietin receptor, useful for diagnosing, preventing or treating  
PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
XX  
XX Claim 10; SEQ ID NO 41; 192pp; English.  
XX  
XX The present invention describes an antibody or its fragment that binds to  
CC or activates an endogenous activity of a human erythropoietin (EPO)  
CC receptor in a mammal, but does not interact with a peptide having a  
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
CC methods of modulating or activating an endogenous activity of a human EPO  
CC receptor in a mammal, comprising administering to the mammal a  
CC therapeutic amount of the above antibody or its fragment to modulate or  
CC activate the receptor; (2) a method of treating a mammal suffering from  
CC aplasia, comprising administering to the mammal a therapeutic amount of  
CC the above antibody or its fragment to modulate or activate the receptor;  
CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
CC an isolated and purified polynucleotide sequence, and their fragments,  
CC complements and degenerate codon equivalents; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antianemic, neuroprotective and vulnerary

CC activities, and can be used in gene therapy. The compositions and methods  
 CC from the present invention can be used for modulating an endogenous  
 CC activity of a human EPO receptor or for treating mammals suffering from  
 CC aplasia or anaemia. They may also be used for identifying mammals having  
 CC a dysfunctional EPO receptor. The composition may also be used in  
 CC promoting wound healing or in protecting against neural cell and/or  
 CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 CC like. The present sequence represents a human anti-EPO-R antibody light  
 CC chain variable region, which is given in the exemplification of the  
 CC present invention.

XX Sequence 107 AA;

Query Match 96.6%; Score 539; DB 8; Length 107;  
 Best Local Similarity 96.3%; Pred. No. 5.2e-33;  
 Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQGVPS 60  
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQGVPS 60  
 QY 61 RFGSGSGTDFTLTISSLPEDFATYYCLOHNSDPCSFQGGTKLEIR 107  
 DB 61 RFGSGSGTDFTLTISSLPEDFATYYCLOHNSYPCSFQGGTKLEIK 107

RESULT 12

ADR68544  
 ID ADR68544 standard; protein; 107 AA.

XX AC ADR68544;

DT 02-DEC-2004 (first entry)

XX Anti-EPO-R-antibody light chain variable region seqid 41.

XX antianaemic; respiratory; vulnery; Gene therapy; vaccine;  
 XX erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
 KW wound healing; neural cell damage; tissue damage; brain injury;  
 KW spinal cord injury; stroke; anti-EPO-R-antibody; light chain;  
 KW variable region.

XX Homo sapiens.

XX US2004175379-A1.

XX 09-SEP-2004.

XX 10-OCT-2003; 2003US-00684109.

XX 14-OCT-2002; 2002US-0418031P.

XX (DEVIR/) DEVRIES P J.

XX (OSTR/) OSTROW D H.

XX (REIL/) REILLY E B.

XX (GREE/) GREEN L L.

XX (WIEL/) WIELER J.

XX Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;

XX WPI; 2004-661369/64.

XX N-PSDB; ADR68543.

XX New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.

XX Claim 10; SEQ ID NO 41; 156pp; English.

XX The invention describes an antibody or its fragment that activates an  
 CC endogenous activity or capable of binding to a human erythropoietin  
 CC receptor in a mammal, or that comprises at least one heavy or light chain

CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 CC given in the specification. Also described are: a method of activating or  
 CC modulating an endogenous activity of a human erythropoietin receptor in a  
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
 CC isolated and purified polynucleotide sequence selected from 28 sequences  
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
 CC the specification, and their fragments, complements, and degenerate codon  
 CC equivalents; and an isolated and purified amino acid sequence selected  
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 CC their fragments. The antibody or its antibody fragment that activates or  
 CC modulates the activity of the receptor is useful in a method of treating  
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
 CC treating disorders characterised by decreased or subnormal levels of  
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 CC reduced blood flow. They are also useful for promoting wound healing or  
 CC for protecting against neural cell and/or tissue damage, resulting from  
 CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 CC useful for identifying or diagnosing mammals having dysfunctional  
 CC erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R  
 CC -antibody light chain variable region.

XX Sequence 107 AA;

Query Match 96.6%; Score 539; DB 8; Length 107;  
 Best Local Similarity 96.3%; Pred. No. 5.2e-33;  
 Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQGVPS 60  
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFTLTISSLPEDFATYYCLOHNSDPCSFQGGTKLEIR 107

DB 61 RFGSGSGTDFTLTISSLPEDFATYYCLOHNSYPCSFQGGTKLEIK 107

RESULT 13

ADS84452

ID ADS84452 standard; protein; 234 AA.

XX AC ADS84452;

XX 18-NOV-2004 (first entry)

XX Human anti-EPO-R antibody Ab390 light chain SEQ ID NO:91.

XX human; erythropoietin receptor; EPO receptor;  
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 KW antianaemic; neuroprotective; vulnery; Gene therapy; aplasia; anaemia;  
 KW wound healing; neural cell damage protection;  
 KW neural tissue damage protection; brain injury; spinal cord injury;  
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.

XX Homo sapiens.

XX WO2004035603-A2.

XX 29-APR-2004.

XX 14-OCT-2003; 2003WO-US032243.

XX 14-OCT-2002; 2002US-00269711.

XX 10-OCT-2003; 2003US-00684109.

XX (ABBO ) ABBOTT LAB.

XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;

DR WPI; 2004-348433/32.  
 DR N-PSDB; ADS84450, ADS84451.  
 XX New antibodies that bind to or activate an endogenous human  
 PT erythropoietin receptor, useful for diagnosing, preventing or treating  
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
 PT anemia.  
 XX  
 PS Disclosure; SEQ ID NO 91; 192pp; English.  
 XX  
 CC The present invention describes an antibody or its fragment that binds to  
 CC or activates an endogenous activity of a human erythropoietin (EPO)  
 CC receptor in a mammal, but does not interact with a peptide having a  
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 CC methods of modulating or activating an endogenous activity of a human EPO  
 CC receptor in a mammal, comprising administering to the mammal a  
 CC therapeutic amount of the above antibody or its fragment to modulate or  
 CC activate the receptor; (2) a method of treating a mammal suffering from  
 CC aplasia, comprising administering to the mammal a therapeutic amount of  
 CC the above antibody or its fragment to modulate or activate the receptor;  
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 CC an isolated and purified polynucleotide sequence, and their fragments,  
 CC complements and degenerate codon equivalents; and (5) an isolated and  
 CC purified amino acid sequence, and their fragments. The EPO receptor  
 CC binding antibody has antianaemic, neuroprotective and vulnerary  
 CC activities, and can be used in gene therapy. The compositions and methods  
 CC from the present invention can be used for modulating an endogenous  
 CC activity of a human EPO receptor or for treating mammals suffering from  
 CC aplasia or anaemia. They may also be used for identifying mammals having  
 CC a dysfunctional EPO receptor. The composition may also be used in  
 CC promoting wound healing or in protecting against neural cell and/or  
 CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 CC like. The present sequence represents a human anti-EPO-R antibody light  
 CC chain, which is given in the exemplification of the present invention.  
 XX  
 SQ Sequence 234 AA;  
 Query Match 96.6%; Score 539; DB 8; Length 234;  
 Best Local Similarity 96.3%; Pred. No. 1.1e-32;  
 Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60  
 DB 21 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 80  
 QY 61 RFGSGSGTDFTLTISLQPEDFATYICLOHNSDPCSFQGTGLEIR 107  
 DB 81 RFGSGSGTDFTLTISLQPEDFATYICLOHNSYPCSFQGTGLEIK 127  
 RESULT 14  
 ADR68594  
 ID ADR68594 standard; protein; 234 AA.  
 XX  
 AC ADR68594;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human antibody Ab390 light chain polypeptide seqid 91.  
 XX  
 KW antianaemic; respiratory; vulnerary; gene therapy; vaccine;  
 KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
 KW wound healing; neural cell damage; tissue damage; brain injury;  
 KW spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;  
 KW AB390; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004175379-A1.  
 XX  
 PD 09-SEP-2004.

XX  
 PF 10-OCT-2003; 2003US-00684109.  
 XX  
 PR 14-OCT-2002; 2002US-0418031P.  
 XX  
 PA (DEVRA/) DEVRIES P J.  
 PA (OSTR/) OSTROW D H.  
 PA (REIL/) REILLY E B.  
 PA (GREE/) GREEN L L.  
 PA (WIEL/) WIELER J.  
 XX  
 XX Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
 XX WPI; 2004-661369/64.  
 DR N-PSDB; ADR68592.  
 DR  
 XX New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.  
 XX  
 PS Disclosure; SEQ ID NO 91; 156pp; English.  
 XX  
 CC The invention describes an antibody or its fragment that activates an  
 CC endogenous activity or capable of binding to a human erythropoietin  
 CC receptor in a mammal, or that comprises at least one heavy or light chain  
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 CC given in the specification. Also described are: a method of activating or  
 CC modulating an endogenous activity of a human erythropoietin receptor in a  
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
 CC isolated and purified polynucleotide sequence selected from 28 sequences  
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
 CC the specification, and their fragments, complements, and degenerate codon  
 CC equivalents; and an isolated and purified amino acid sequence selected  
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 CC their fragments. The antibody or its antibody fragment that activates or  
 CC modulates the activity of the receptor is useful in a method of treating  
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
 CC treating disorders characterised by decreased or subnormal levels of  
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 CC reduced blood flow. They are also useful for promoting wound healing or  
 CC for protecting against neural cell and/or tissue damage, resulting from  
 CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 CC useful for identifying or diagnosing mammals having dysfunctional  
 CC erythropoietin receptor. This sequence represents a human Ab390 antibody  
 CC heavy chain polynucleotide.  
 XX  
 SQ Sequence 234 AA;  
 Query Match 96.6%; Score 539; DB 8; Length 234;  
 Best Local Similarity 96.3%; Pred. No. 1.1e-32;  
 Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60  
 DB 21 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 80  
 QY 61 RFGSGSGTDFTLTISLQPEDFATYICLOHNSDPCSFQGTGLEIR 107  
 DB 81 RFGSGSGTDFTLTISLQPEDFATYICLOHNSYPCSFQGTGLEIK 127  
 RESULT 15  
 ADK18841  
 ID ADK18841 standard; protein; 107 AA.  
 XX  
 AC ADK18841;  
 XX  
 DT 06-MAY-2004 (first entry)



XX Anti-human PDGF-D antibody protein related sequence #67.  
DE antiinflammatory; immunomodulator; cytostatic; gene therapy.  
KW Homo sapiens.  
OS WO2003057857-A2.  
PN 17-JUL-2003.  
XX 06-JAN-2003; 2003WO-US000398.  
XX 07-JAN-2002; 2002US-00041860.  
XX (ABGE-) ABGENIX INC.  
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
FI Bezabeh B;  
XX WPI; 2003-587119/55.  
XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX Disclosure; SEQ ID NO 265; 255pp; English.  
XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX Sequence 107 AA;

Query Match 94.6%; Score 528; DB 7; Length 107;  
Best Local Similarity 95.3%; Pred. No. 3.5e-32;  
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 DIQWTQSPSLASVGDRTVITCRASQGIKNDLQWYQKPKAPKRLIYAASLSQGVPS 60  
Db 1 DIQWTQSPSLASVGDRTVITCRASQGIKNDLQWYQKPKAPKRLIYAASLSQGVPS 60  
Qy 61 RFSGSGGTDTLTITSSLPEDFATYYCLOHNSDPCSFQGTGLEIR 107  
Db 61 RFSGSGGTDTLTITSSLPEDFATYYCLOHNSYPWTFQGTGLEIK 107

Search completed: April 25, 2007, 04:05:19  
Job time : 93.7938 secs



GenCore version 6.2.1

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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 8 Seconds  
(without alignments)  
1261.509 Million cell updates/sec

Title: US-10-665-383-24

Perfect score: 558

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLQHNSDPCSPFGQGTKLEIR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	89.8	125	2 S40353	Ig kappa chain V-J
2	494	88.5	108	1 KIHUGL	Ig kappa chain V-I
3	489	87.6	108	1 KIHUEU	Ig kappa chain V-I
4	488	87.5	123	2 S40313	Ig kappa chain V-J
5	484	86.7	107	2 S36269	Ig lambda chain V
6	481	86.2	117	2 S41809	Ig kappa chain V r
7	480	86.0	107	2 S36262	Ig lambda chain V
8	471	84.4	129	2 S40369	Ig kappa chain - h
9	468	83.9	123	2 S40331	Ig kappa chain - h
10	467	83.7	127	2 S40367	Ig kappa chain V-J
11	466	83.5	126	2 S40335	Ig kappa chain V-J
12	463	83.0	108	2 S36275	Ig lambda chain V
13	463	83.0	108	2 B49047	Ig kappa chain V r
14	461	82.6	131	2 S40352	Ig kappa chain V-J
15	460	82.4	114	2 S46377	Ig kappa chain V-J
16	459	82.3	125	2 S40333	Ig kappa chain V-J
17	456	81.7	108	2 S19674	Ig kappa chain V r
18	455.5	81.6	107	2 S36275	Ig lambda chain V
19	455	81.5	108	1 KIHUHU	Ig kappa chain V r
20	455	81.5	125	2 S40349	Ig kappa chain V-J
21	454	81.4	95	2 S69898	Ig kappa chain V r
22	453	81.2	132	2 S40334	Ig kappa chain - h
23	452	81.0	117	2 S42264	Ig kappa chain V r
24	451	80.8	117	2 S46376	Ig kappa chain V-J
25	450.5	80.7	107	2 S47183	Ig kappa chain - h
26	449	80.5	107	2 I69017	anti-HIV1 envelope
27	449	80.5	129	1 KIHUWK	Ig kappa chain pre
28	447.5	80.2	124	2 S40336	Ig kappa chain V-J
29	447	80.1	107	2 S36264	Ig lambda chain V

30	447	80.1	108	1 KIHUEU	Ig kappa chain V-I
31	447	80.1	108	2 S47182	Ig kappa chain - h
32	447	80.1	129	2 S52793	Ig kappa chain V r
33	446	79.9	108	1 KIHUBN	Ig kappa chain V-I
34	446	79.9	129	2 S40317	Ig kappa chain - h
35	445	79.7	105	2 S36266	Ig lambda chain V
36	445	79.7	117	2 S46371	Ig kappa chain V-J
37	444	79.6	108	2 S44122	Ig kappa chain V r
38	444	79.6	122	2 S40314	Ig kappa chain - h
39	443.5	79.5	108	2 S30521	Ig kappa chain V r
40	443	79.4	120	2 S46370	Ig kappa chain V-J
41	442	79.2	117	2 C21056	Ig kappa chain pre
42	441	79.0	124	2 S40318	Ig kappa chain V r
43	441	79.0	128	2 S46372	Ig light chain var
44	438	78.5	129	2 S52789	Ig kappa chain V r
45	437	78.3	109	2 S31998	Ig kappa chain - h

## ALIGNMENTS

## RESULT 1

S40353

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C&gt;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40353

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40353

A&gt;Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 &lt;KLE&gt;

A:Cross-references: UNIPARC:UPI0000176CAB; EMBL:X72463

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

P:30-104/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 89.8%; Score 501; DB 2; Length 125;  
Best Local Similarity 89.7%; Pred. No. 3.2e-36;  
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGTRNDLQWYQKPGKAPKRLIYAASSLSQSGVPS 60

DB 15 DIQMTQSPSSLSASVGRVTITCRASQIGTRNDLQWYQKPGKAPKRLIYAASSLSQSGVPS 74

QY 61 RFSGSGSGTDFTLTITSSLPQEDPATYCYCLQHNSDPCSPFGQGTKLEIR 107

DB 75 RFSGSGSGTEFTLTITSLQPEDPATYCYCLQHNSDPCSPFGQGTKLEIR 121

## RESULT 2

KIHUGL

Ig kappa chain V-I region (Gal) - human (tentative sequence)

C:Species: Homo sapiens (man)

C&gt;Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004

C:Accession: A01867

R:Laure, C.J.; Watanabe, S.; Hilachmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973

A:Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I,

A:Reference number: A01867; MUID:75059122; PMID:4215718

A:Accession: A01867

A:Molecule type: protein

A:Residues: 1-108 &lt;LAU&gt;

A:Cross-references: UNIPROT:P01599; UNIPARC:UPI000012E142

A&gt;Note: The C region of this chain has the Inv (3) marker

C:Comment: This chain was isolated from a Waldenstrom's macroglobulin.

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-90/Domain: immunoglobulin homology <IMM>  
 F:23-88/Disulfide bonds: #status predicted

Query Match 88.5%; Score 494; DB 1; Length 108;  
 Best Local Similarity 89.7%; Pred. No. 1.1e-35;  
 Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTITSSLPQDFATYICLQHNSDPCSFQGGTKLEIR 107

Db 61 RFGSGSGTDFTLTITSSLPQDFATYICLQHNSDPCSFQGGTKLEIR 107

#### RESULT 3

KLHWE

Ig kappa chain V-I region (WEA) - human

C:Species: Homo sapiens (man)

C:Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004

C:Accession: A01876

R:Goni, F.; Frangione, B.

Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983

A:Title: Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) with

A:Reference number: A93964; MUID:83273707; PMID:6410398

A:Accession: A01876

A:Molecule type: protein

A:Residues: 1-108 <CON>

A:Cross-references: UNIPROT:P01610; UNIPARC:UPI000012E14C

C:Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated galactose

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-90/Domain: immunoglobulin homology <IMM>  
 F:23-88/Disulfide bonds: #status predicted

Query Match 87.6%; Score 489; DB 1; Length 108;  
 Best Local Similarity 86.9%; Pred. No. 3e-35;  
 Matches 93; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPGTAPKRLIYGATSLQSGVPS 60

Qy 61 RFGSGSGTDFTLTITSSLPQDFATYICLQHNSDPCSFQGGTKLEIR 107

Db 61 RFGSGSGTDFTLTITSSLPQDFATYICLQHNSDPCSFQGGTKLEIR 107

#### RESULT 4

S40313

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40313

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40313

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KUE>

A:Cross-references: UNIPARC:UPI000011613F; EMBL:X72423; NID:9441314; PIDN:CAAS1091.1; PII  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 488; DB 2; Length 123;  
 Best Local Similarity 87.9%; Pred. No. 4.1e-35;  
 Matches 94; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

Db 17 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 76

Qy 61 RFGSGSGTDFTLTITSSLPQDFATYICLQHNSDPCSFQGGTKLEIR 107

Db 77 RFGSGSGTDFTLTITSSLPQDFATYICLQHNSDPCSFQGGTKLEIR 123

#### RESULT 5

S36269

Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000

C:Accession: S36269

R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;

EMBO J. 12, 725-734, 1993

A:Title: Human anti-self antibodies with high specificity from phage display libraries.

A:Reference number: S36256; MUID:93178448; PMID:7679990

A:Accession: S36269

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-107 <GRI>

A:Cross-references: UNIPARC:UPI0000118DF1; EMBL:Z18838; NID:933422; PIDN:CAA79290.1; PID:

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 484; DB 2; Length 107;  
 Best Local Similarity 88.8%; Pred. No. 8e-35;  
 Matches 95; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPGKAPKRLIYTSSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTITSSLPQDFATYICLQHNSDPCSFQGGTKLEIR 107

Db 61 RFGSGSGTDFTLTITSSLPQDFATYICLQHNSDPCSFQGGTKLEIR 107

#### RESULT 6

S41809

Ig kappa chain V region A30 - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S41809

R:Huber, C.; Schaeuble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Zacht

Eur. J. Immunol. 23, 2868-2875, 1993

A:Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequence

A:Reference number: S41809; MUID:94039386; PMID:8223863

A:Accession: S41809

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-117 <HUB>

A:Cross-references: UNIPARC:UPI000011618B; EMBL:X72808; NID:9415383; PIDN:CAAS1328.1; PII

C:Genetics:

A:Introns: 19/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 481; DB 2; Length 117;  
 Best Local Similarity 97.9%; Pred. No. 1.6e-34;

Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITICRISQGIIRNDLGYQKPGKAPKRLIYAASSLSQGVPS 60  
 |||||  
 Db 23 DIQMTQSPSSLSASVGDRTVITICRISQGIIRNDLGYQKPGKAPKRLIYAASSLSQGVPS 82  
 |||||  
 QY 61 RPSGSGSGTDFLTITSSLOPEDFATYICLQHNSDP 95  
 |||||  
 Db 83 RPSGSGSGTDFLTITSSLOPEDFATYICLQHNSTP 117  
 |||||

## RESULT 7

S36262  
 Ig lambda chain V region (clone alpha-TNF-E7) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
 C:Accession: S36262  
 R:Griffiths, A.D.; Malnqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
 EMBO J. 12, 725-734, 1993  
 A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A:Reference number: S36256; MUID:93178448; PMID:7679990  
 A:Accession: S36262  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <GRI>  
 A:Cross-references: UNIPARC:UPI0000176D2C; EMBL:Z18842  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 480; DB 2; Length 107;  
 Best Local Similarity 87.9%; Pred. No. 1.8e-34;  
 Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITICRISQGIIRNDLGYQKPGKAPKRLIYAASSLSQGVPS 60  
 |||||  
 Db 1 DIQMTQSPSSLSASVGDRTVITICRISQGIIRNDLGYQKPGKAPKRLIYAASSLSQGVPS 60  
 |||||  
 QY 61 RPSGSGSGTDFLTITSSLOPEDFATYICLQHNSDP 107  
 |||||  
 Db 61 RPSGSGSGTDFLTITSSLOPEDFATYICLQHNSTP 107  
 |||||

## RESULT 8

S40369  
 Ig kappa chain - human  
 C:Species: Homo sapiens (man)  
 C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S40369  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40312; MUID:94080891; PMID:8258341  
 A:Accession: S40369  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-129 <KLS>  
 A:Cross-references: UNIPARC:UPI0000116177; EMBL:X72479; NID:9441426; PIDN:CAA51147.1; PI  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 471; DB 2; Length 129;  
 Best Local Similarity 86.9%; Pred. No. 1.2e-33;  
 Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITICRISQGIIRNDLGYQKPGKAPKRLIYAASSLSQGVPS 60  
 |||||  
 Db 22 DIQMTQSPSSLSASVGDRTVITICRASHVISNHLVNFQKPGKAPKSLIYAASSLSQGVPS 81  
 |||||  
 QY 61 RPSGSGSGTDFLTITSSLOPEDFATYICLQHNSDP 107  
 |||||  
 Db 82 RPSGSGSGTDFLTITSSLOPEDFATYICLQHNSTP 128  
 |||||

## RESULT 9

S40331  
 Ig kappa chain - human  
 C:Species: Homo sapiens (man)  
 C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S40331  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40312; MUID:94080891; PMID:8258341  
 A:Accession: S40331  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-123 <KLE>  
 A:Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PI  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 468; DB 2; Length 123;  
 Best Local Similarity 86.9%; Pred. No. 2.1e-33;  
 Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITICRISQGIIRNDLGYQKPGKAPKRLIYAASSLSQGVPS 60  
 |||||  
 Db 17 DIQMTQSPSSLSASVGDRTVITICRISQGIIRNDLGYQKPGKAPKRLIYAASSLSQGVPS 76  
 |||||  
 QY 61 RPSGSGSGTDFLTITSSLOPEDFATYICLQHNSDP 107  
 |||||  
 Db 77 RPSGSGSGTDFLTITSSLOPEDFATYICLQHNSTP 123  
 |||||

## RESULT 10

S40367  
 Ig kappa chain V-J-C region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S40367  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40312; MUID:94080891; PMID:8258341  
 A:Accession: S40367  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-127 <KLE>  
 A:Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 467; DB 2; Length 127;  
 Best Local Similarity 86.0%; Pred. No. 2.7e-33;  
 Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITICRISQGIIRNDLGYQKPGKAPKRLIYAASSLSQGVPS 60  
 |||||  
 Db 18 DIQMTQSPSSLSASVGDRTVITICRISQGIIRNDLGYQKPGKAPKRLIYAASSLSQGVPS 77  
 |||||  
 QY 61 RPSGSGSGTDFLTITSSLOPEDFATYICLQHNSDP 107  
 |||||  
 Db 78 RPSGSGSGTDFLTITSSLOPEDFATYICLQHNSTP 124  
 |||||

## RESULT 11

S40335  
 Ig kappa chain V-J-C region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S40335  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Query Match 83.0%; Score 463; DB 2; Length 108;  
Best Local Similarity 86.0%; Pred. No. 5.1e-33;  
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTPSSLSASVGRVTITCRASQGIRNDIGWYQQKPGAKPELLIYAASSLQGVPS 60  
Db 1 DIQMTPSSLSASVGRVTITCRASQSISLYNWTQQKPGAKLLIIYAASSLQGVPS 60

RESULT 14  
S40352  
IG kappa chain V-J-C region - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #Text\_change 2  
C;Accession: S40352

```

61 RFSGSGSGTDFWLTITSSLPQEDFATYCLQHNSDPCSFQGGTKLEIR 107
      |||||
81 RFSGSGSGTDFSLTITSSLPQEDVATYICQKYNVPRTFQGGTKVEIK 127
      |||||

RESULT 15
S46377
```

RESULT 13  
B49047  
IG kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragment)  
C; Species: Homo sapiens (man)  
C; Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C; Accession: B49047  
R; Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.  
Eur. J. Immunol. 22, 2231-2236, 1992  
A; Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes  
A; Reference number: A49047; PMID:92387224; PMID:1516616  
A; Accession: B49047  
A; Status: preliminary  
A; Molecule type: nucleic acid  
A; Residues: 1-108 <VIC>  
A; Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000175B44  
A; Experimental source: thymic B lymphocytes

RESULT 13  
B49047  
IG kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragment)  
C; Species: Homo sapiens (man)  
C; Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C; Accession: B49047  
R; Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.  
Eur. J. Immunol. 22, 2231-2236, 1992  
A; Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes  
A; Reference number: A49047; PMID:92387224; PMID:1516616  
A; Accession: B49047  
A; Status: preliminary  
A; Molecule type: nucleic acid  
A; Residues: 1-108 <VIC>  
A; Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000175B44  
A; Experimental source: thymic B lymphocytes

Db 8 IQMRQSPSSLSASVGRVTITCRASQIRNDLGWNQKPKAPKLLIYAASSLESQVPSR 67

Qy 62 FSGSGTDFTLTISSLOPEDPATYCYLQHNSDPCSFQGTKEI 106

Db 68 FSGSGTDFTLTISSLOPEDPATYCYLQDYSYPLTFGGGTRKWI 112

Search completed: April 25, 2007, 04:06:39  
Job time : 9.16102 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 73 Seconds  
(without alignments)  
1574.822 Million cell updates/sec

Title: US-10-665-383-24

Perfect score: 558

Sequence: 1 DQMTQSPSSLSASVGRVT.....CLQNSDPCSFQGTKLEIR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_8.4.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	511	91.6	236	2	Q502W4 HUMAN	Q502W4 homo sapien
2	494	88.5	108	1	KV1G HUMAN	P01599 homo sapien
3	490	87.8	236	2	Q6GMW1 HUMAN	Q6gmw1 homo sapien
4	489	87.6	108	1	KV1R_HUMAN	P01610 homo sapien
5	459	84.1	108	2	Q9UL70 HUMAN	Q9ul70 homo sapien
6	462	82.8	236	2	Q6GMX8 HUMAN	Q6gmx8 homo sapien
7	456	81.7	236	2	Q7Z3Y4 HUMAN	Q7z3y4 homo sapien
8	455	81.5	108	1	KV1H_HUMAN	P01600 homo sapien
9	453	81.2	108	2	Q9UL77_HUMAN	Q9ul77 homo sapien
10	453	81.2	236	2	Q6FIH7_HUMAN	Q6phi7 homo sapien
11	449	80.5	129	1	KV1W_HUMAN	P04431 homo sapien
12	447	80.1	108	1	KV1F_HUMAN	P01598 homo sapien
13	446	79.9	108	1	KV1V_HUMAN	P04430 homo sapien
14	445.5	79.8	107	2	Q9SA9 HUMAN	Q9esa9 homo sapien
15	445	79.7	244	2	Q6SZC8 HUMAN	P01600 homo sapien
16	440	78.9	236	2	Q6GMX9 HUMAN	Q6gmx9 homo sapien
17	440	78.9	236	2	Q6GMX0 HUMAN	Q6gmxx0 homo sapien
18	437	78.3	240	2	Q6SZC9 HUMAN	Q6szc9 homo sapien
19	434.5	77.9	107	2	Q9UL81_HUMAN	Q9ul81 homo sapien
20	431	77.2	108	1	KV1O_HUMAN	P01607 homo sapien
21	430	77.1	234	2	QSEFE6 HUMAN	Qsefe6 homo sapien
22	429	76.9	108	2	Q9UL79_HUMAN	Q9ul79 homo sapien
23	429	76.9	236	2	Q6PIT5 HUMAN	Q6pit5 homo sapien
24	427	76.5	108	1	KV1N_HUMAN	P01606 homo sapien
25	427	76.5	117	1	KV1I_HUMAN	P01601 homo sapien
26	426	76.3	108	1	KV1C_HUMAN	P01595 homo sapien
27	426	76.3	108	1	KV1E_HUMAN	P01597 homo sapien
28	426	76.3	236	2	Q6PIH4 HUMAN	Q6phi4 homo sapien
29	425	76.2	108	1	KV1M_HUMAN	P01605 homo sapien
30	425	76.2	108	1	KV1Q_HUMAN	P01609 homo sapien
31	424	76.0	108	1	KV1S_HUMAN	P01611 homo sapien

32	423	75.8	108	1	KV1B_HUMAN	P01594 homo sapien
33	423	75.8	108	1	KV1D_HUMAN	P80362 homo sapien
34	419.5	75.2	107	1	KV1D_HUMAN	P01596 homo sapien
35	418	74.9	108	1	KV1L_HUMAN	P01604 homo sapien
36	418	74.9	234	2	Q7Z473_HUMAN	Q7z473 homo sapien
37	416	74.6	108	1	KV1A_HUMAN	P01593 homo sapien
38	416	74.6	108	1	KV1K_HUMAN	P01603 homo sapien
39	415	74.4	108	1	KV1P_HUMAN	P01608 homo sapien
40	410	73.5	117	1	KV1J_HUMAN	P01602 homo sapien
41	410	73.5	129	1	KV1X_HUMAN	P04432 homo sapien
42	405	72.6	189	2	Q569I7_HUMAN	Q569i7 homo sapien
43	397	71.1	108	1	KV5S_MOUSE	P01652 mus musculus
44	396	71.0	116	2	Q96PF6_HUMAN	Q96pf6 homo sapien
45	395.5	70.9	109	1	KV1T_HUMAN	P01612 homo sapien

## ALIGNMENTS

### RESULT 1

Q502W4\_HUMAN PRELIMINARY; PRT; 236 AA.  
AC Q502W4;

DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.

DT 07-JUN-2005, sequence version 1.

DT 11-JUL-2006, entry version 13.

DE IGKC protein.

GN Name=IGKC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Glandular pool- thyroid;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Glandular pool- thyroid;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major

histocompatibility complex class I molecules (By similarity).

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EMBL; BC095489; AAH95489.1; -; mRNA.

DR SMR; Q502W4; 23-236.

DR Ensemble; ENSG00000163245; Homo sapiens.

DR GO; GO:0016021; C-integral to membrane; IEA.

DR GO; GO:0016020; C-membrane; IEA.

DR GO:0030106; F:MHC class I receptor activity; IEA.  
 DR GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
 DR GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_C1-set.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003599; Ig\_sub.  
 DR InterPro: IPR013106; Ig V-set.  
 DR InterPro: IPR003596; Ig V-set\_sub.  
 DR Pfam: PF07654; C1-set; 1.  
 DR Pfam: PF07686; V-set; 1.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00407; IGc1; 1.  
 DR SMART: SM00406; IGv; 1.  
 DR PROSITE: PS0835; IG LIKE; 2.  
 DR PROSITE: PS0290; IG\_MHC; UNKNOWN 1.  
 KW Immunoglobulin domain; Membrane; Repeat; Transmembrane.  
 SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query Match 91.6%; Score 511; DB 2; Length 236;  
 Best Local Similarity 91.6%; Pred. No. 2, 1e-44;  
 Matches 98; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGYQKPGKPKRLIYAASSLSQGVPS 60  
 Db 23 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGYQKPGKPKRLIYAASSLSQGVPS 82  
 QY 61 RFGSGSGTDTLTITSLQPEDFATYICLQHNSDPCSFQGTKEIR 107  
 Db 83 RFGSGSGTDTLTITSLQPEDFATYICLQNSYPRTEFGQTKVEIK 129

RESULT 2  
 KVIG HUMAN STANDARD; PRT; 108 AA.  
 AC P01599;  
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
 DT 21-JUL-1986, sequence version 1.  
 DT 25-JUN-2006, entry version 43.  
 DE Ig kappa chain V-I region Gal.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=75059122; PubMed=4215718;  
 RA Laure C.J., Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal IgM-immunoglobulin  
 (macroglobulin Gal.), I. The amino acid sequence of the L-chain of  
 kappa-type, subgroup I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).  
 CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -!- MISCELLANEOUS: This chain was isolated from a Waldenström's  
 macroglobulin.  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC  
 CC PIR: A01867; K1HUGL.  
 DR HSSP; P01607; 1BWW.  
 DR SMR; P01599; 1-108.  
 DR GO:0005576; C:extracellular region; NAS.  
 DR GO:0003823; P:antigen binding; NAS.  
 DR GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003599; Ig\_sub.  
 DR InterPro: IPR013106; Ig V-set.  
 DR InterPro: IPR003596; Ig V-set\_sub.  
 DR Pfam: PF07686; V-set; 1.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00406; IGv; 1.

DR PROSITE; PS0835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT CHAIN 1 >108  
 FT Ig kappa chain V-I region Gal.  
 FT /FTID=PRO 0000059743.  
 FT FRAMEWORK-1.  
 FT REGION 1 23  
 FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 107  
 FT DIULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 88.5%; Score 494; DB 1; Length 108;  
 Best Local Similarity 89.7%; Pred. No. 4, 9e-43;  
 Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGYQKPGKPKRLIYAASSLSQGVPS 60  
 Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGYQKPGKPKRLIYAASSLSQGVPS 60  
 QY 61 RFGSGSGTDTLTITSLQPEDFATYICLQHNSDPCSFQGTKEIR 107  
 Db 61 RFGSGSGTDTLTITSLQPEDFATYICLQNSYPRTEFGQTKVEIK 107

RESULT 3  
 Q6GMW1 HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6GMW1;  
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2004, sequence version 1.  
 DT 27-JUN-2006, entry version 22.  
 DE IGKC protein.  
 DE IGKC protein.  
 GN Name=IGKC;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Viallon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major

```

CC      histocompatibility complex class I molecules (By similarity).
CC      -----
CC      Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL: BC073791; AAH73791.1; -; mRNA.
DR      SMR: Q6GWW1; 24-236.
DR      Ensembl: ENSG00000163245; Homo sapiens.
DR      GO: GO:0016021; C:integral to membrane; IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0030106; F:MHC class I receptor activity; IEA.
DR      GO: GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR      GO: GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR      InterPro: IPR007110; IG-like.
DR      InterPro: IPR003597; IG C1-set.
DR      InterPro: IPR003006; IG_MHC.
DR      InterPro: IPR003599; IG_sub.
DR      InterPro: IPR013106; IG_V-set.
DR      Pfam: PF07654; C1-set; 1.
DR      Pfam: PF07686; V-set; 1.
DR      SMART: SM00409; IG; 1.
DR      SMART: SM00407; IGL1; 1.
DR      SMART: SM00406; IGV; 1.
DR      PROSITE: PS00835; IG LIKE; 2.
DR      PROSITE: PS00290; IG_MHC; UNKNOWN 1.
KW      Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SQ      SEQUENCE 236 AA; 25751 MW; 5BP56A087APAC437 CRC64;

Query Match      87.8%; Score 490; DB 2; Length 236;
Best Local Similarity 90.6%; Pred. No. 3.1e-42;
Matches 96; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      2 IQWTSPSSLSASVGRVITTCRASQGIKNDLQWYQKPGKAPKRLIYAASSLSQGVPSR 61
DB      24 IQWTSPSSLSASVGRVITTCRASQGIKNDLQWYQKPGKAPKRLIYAASSLSQGVPSR 83
QY      62 FSGSGSGTDTLTITSLQPEDFATYYCLOHNSDPCSFQGTQKLEIR 107
DB      84 FSGSGSGTDTLTITSLQPEDFATYYCLOHNSDPCSFQGTQKLEIR 129

RESULT 4
KVLR_HUMAN
ID      KVLR_HUMAN STANDARD; PRT; 108 AA.
AC      P01610;
DT      21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT      21-JUL-1986, sequence version 1.
DT      30-MAY-2006, entry version 39.
DE      Ig kappa chain V-I region WEA.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      PROTEIN SEQUENCE.
RX      MEDLINE=83273707; PubMed=6410398;
RA      Goni F., Frangione B.;
RT      "Amino acid sequence of the Fv region of a human monoclonal IgM
RT      (protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT      in Klebsiella polysaccharides K30 and K33.";
RL      Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC      -!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC      against 3,4-pyruvylated galactose and isolated from a patient with
CC      Waldenstrom's macroglobulinemia.
CC      -----
CC      Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      PIR: A01876; KIHUWE.
DR      HSSP: P80362; 1WTI.
DR      SMR: P01610; 1-108.

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DR      GO: GO:0005576; C:extracellular region; NAS.
DR      GO: GO:0003823; F:antigen binding; NAS.
DR      GO: GO:0006955; P:immune response; NAS.
DR      InterPro: IPR007110; IG-like.
DR      InterPro: IPR003599; IG_sub.
DR      InterPro: IPR013106; IG_V-set.
DR      InterPro: IPR003596; IG_V-set_sub.
DR      Pfam: PF07686; V-set; 1.
DR      SMART: SM00409; IG; 1.
DR      SMART: SM00406; IGV; 1.
DR      PROSITE: PS00835; IG LIKE; 1.
KW      Direct protein sequencing; Immunoglobulin domain;
KW      Immunoglobulin V region; Monoclonal antibody.
FT      CHAIN 1 >108
FT      /FTID=PRO_0000059752.
FT      REGION 1 23 Framework-1.
FT      REGION 24 34 Complementarity-determining-1.
FT      REGION 35 49 Framework-2.
FT      REGION 50 56 Complementarity-determining-2.
FT      REGION 57 88 Framework-3.
FT      REGION 89 97 Complementarity-determining-3.
FT      REGION 98 107 Framework-4.
FT      DISULFID 23 88 By similarity.
FT      NON_TER 108
SQ      SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match      87.6%; Score 489; DB 1; Length 108;
Best Local Similarity 86.9%; Pred. No. 1.6e-42;
Matches 93; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY      1 DIQWTSPSSLSASVGRVITTCRASQGIKNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
DB      1 DIQWTSPSSLSASVGRVITTCRASQGIKNDLQWYQKPGKAPKRLIYGATSLQGVPS 60
QY      61 RFSGSGSGTDTLTITSLQPEDFATYYCLOHNSDPCSFQGTQKLEIR 107
DB      61 RFSGSGSGTDTLTITSLQPEDFATYYCLOHNSDPCSFQGTQKLEIR 107

RESULT 5
Q9UL70_HUMAN
ID      Q9UL70_HUMAN PRELIMINARY; PRT; 108 AA.
AC      Q9UL70;
DT      01-MAY-2000, integrated into UniProtKB/TREMBL.
DT      01-MAY-2000, sequence version 1.
DT      18-APR-2006, entry version 23.
DE      Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
RA      Manheimer-Lory A., Katz J.B., Pillinger M., Grossein C., Smith A.,
RA      Diamond B.;
RT      "Molecular characteristics of antibodies bearing an anti-DNA-
RT      associated idiotype.";
RL      J. Exp. Med. 174:1639-1652(1991).
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CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL: AF035044; AAD56280.1; -; mRNA.

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skeletal Muscle;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
 CC histocompatibility complex class I molecules (By similarity).  
 CC  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC  
 CC EMBL: BC005332; AAH05332.1; -; mRNA.  
 DR HSSP; P01834; IHEZ.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig C1-set.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003599; Ig\_sub.  
 DR InterPro; IPR013106; Ig\_V-set.  
 DR InterPro; IPR003596; Ig\_V-set\_sub.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IGc1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;  
 KW Transmembrane.  
 SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;  
 Query Match 81.7%; Score 456; DB 2; Length 236;  
 Best Local Similarity 84.1%; Pred.No.1e-38;  
 Matches 90; Conservative 5; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60  
 Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 82  
 QY 61 RFSGSGSGTDFLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107  
 Db 83 RFSGSGSGTDFLTITSSLOPEDPATYCYCQYKSPVPTFGQGTKEIK 129  
 RESULT 8  
 KV1H\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01600;  
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
 DT 21-JUL-1986, sequence version 1.  
 DT 25-JUL-2006, entry version 47.  
 DE Ig kappa chain V-I region Hau.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=71032830; PubMed=4097974;  
 RA Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-

RT chain of subgroup I (Bence-Jones protein Hau): subdivision within  
 RT subgroups.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC  
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 CC  
 CC PIR; A01868; KIHUHU.  
 DR PDB; 1F6L; X-ray; L=1-89.  
 DR SMR; P01600; 1-108.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003599; Ig\_sub.  
 DR InterPro; IPR013106; Ig\_V-set.  
 DR InterPro; IPR003596; Ig\_V-set\_sub.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin domain; Immunoglobulin V region.  
 FT CHAIN 1 >108  
 FT REGION 1 23  
 FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 107  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 FT STRAND 4 7  
 FT STRAND 9 12  
 FT STRAND 15 16  
 FT STRAND 19 27  
 FT STRAND 30 31  
 FT STRAND 33 38  
 FT STRAND 40 41  
 FT STRAND 45 49  
 FT STRAND 50 52  
 FT STRAND 53 54  
 FT STRAND 56 57  
 FT STRAND 60 61  
 FT STRAND 62 67  
 FT STRAND 68 69  
 FT STRAND 70 75  
 FT STRAND 77 77  
 FT HELIX 80 82  
 FT STRAND 84 90  
 FT STRAND 92 95  
 FT STRAND 98 98  
 FT STRAND 102 105  
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;  
 Query Match 81.5%; Score 455; DB 1; Length 108;  
 Best Local Similarity 84.1%; Pred.No.5.3e-39;  
 Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;  
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 Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQIRNDLGMWYQKPKAPKRLIYAASSLSQSGVPS 60  
 QY 61 RFSGSGSGTDFLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107  
 Db 61 RFSGSGSGTDFLTITSSLOPEDPATYCYCQYKSPVPTFGQGTKEIK 107  
 RESULT 9

Q9UL77 HUMAN  
ID Q9UL77 HUMAN PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DT 23-JUN-2006, entry version 23.  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92387224; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe F.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92387224; PubMed=1516616;  
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;  
RT "Human monoclonal striational autoantibodies isolated from thymic B  
RT lymphocytes of patients with myasthenia gravis use VH and VL gene  
RT segments associated with the autoimmune repertoire.";  
RL Eur. J. Immunol. 22:2231-2236(1992).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93170387; PubMed=8436174;  
RA Wagner S.D., Luzzatto L.;  
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
RT distributed over a large portion of the V kappa locus and do not show  
RT somatic mutation.";  
RL Eur. J. Immunol. 23:391-397(1993).  
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CC  
EMBL; AF035037; AAD56273.1; -; mRNA.  
DR PIR; B49047; B49047.  
DR PIR; S34083; S34083.  
DR HSP; P01607; 1BW6.  
DR SMR; Q9UL77; 1-108.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR RZPD-ProtExp; IOH14191; -.  
DR RZPD-ProtExp; IOH21663; -.  
DR RZPD-ProtExp; IOH23035; -.  
DR RZPD-ProtExp; IOH23055; -.  
DR RZPD-ProtExp; IOH23077; -.  
DR RZPD-ProtExp; IOH23168; -.  
DR RZPD-ProtExp; IOH23177; -.  
DR RZPD-ProtExp; IOH23178; -.  
DR RZPD-ProtExp; IOH23179; -.  
DR RZPD-ProtExp; IOH29440; -.  
DR RZPD-ProtExp; IOH40810; -.  
DR RZPD-ProtExp; IOH7177; -.  
DR RZPD-ProtExp; T2893; -.  
DR RZPD-ProtExp; T2896; -.  
DR RZPD-ProtExp; T2901; -.  
DR RZPD-ProtExp; T2902; -.  
DR RZPD-ProtExp; W0370; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig sub.  
DR InterPro; IPR013106; Ig\_V-set.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
KW Immunoglobulin domain.  
FT NON\_TER 1

FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;  
Query Match 81.2%; Score 453; DB 2; Length 108;  
Best Local Similarity 84.1%; Pred. No. 8.6e-39;  
Matches 90; Conservative 5; Mismatches 12; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKRDNLGWYQKPGKAPKRLIYAASLSQSGVPS 60  
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSISSVLYNWYQKPGKAPNLLIYAASLSQSGVPS 60  
QY 61 RFSGSGGTDFLTITSSLPEDPATYICLQHNSDPCSPGQGTKEIR 107  
DB 61 RFSGSGGTDFLTITSSLPEDPATYICQSYSTSWTFGEGTKVEIK 107  
RESULT 10  
Q6PIH7 HUMAN  
ID Q6PIH7 HUMAN PRELIMINARY; PRT; 236 AA.  
AC Q6PIH7;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 25-JUL-2006, entry version 23.  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Hopkins R.F., Jordan H., Moore T., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Diatchenko L., Marusina K., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RG NIH MGC Project;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
CC histocompatibility complex class I molecules (By similarity).  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
EMBL; BC034141; AAH34141.1; -; mRNA.  
DR PDB; 2AJ3; X-ray; A/C/E-25-236.  
DR SMR; Q6PIH7; 23-236.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.

GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig C1-set.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003599; Ig\_sub.

DR InterPro; IPR013106; Ig\_V-set.

DR InterPro; IPR003596; Ig\_V-set\_sub.

DR Pfam; PF07654; C1-set; 1.

DR Pfam; PF07686; V-set; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00407; IGc1; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS00835; IG\_LIKE; 2.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.

KW Immunoglobulin domain; Membrane; Repeat; Transmembrane.

SEQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 81.2%; Score 453; DB 2; Length 236;

Best Local Similarity 83.2%; Pred.No. 2.le-38;

Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTSPSLSASVGDVRVITTCRASGIGRNDLGGWYQCKPKAPKRLIYAASSIQSGVPS 60

DB 23 DIQTQSPFLSASVGDVRVITTCRASGIGISYLAWYQCKPKAPNLILIYAASLTQSGVPS 82

QY 61 RFGSGSGDFTLTITSSLOPEDFATYYCLOHNSDPCSFQGGTKLEIR 107

DB 83 RFGSGSGTEFTLTITSSLOPEDFATYYCQQLNSPPTFGGTVKEIK 129

RESULT 11

KV1W HUMAN

ID KV1W HUMAN STANDARD; PRT; 129 AA.

AC P04431;

DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.

DT 13-AUG-1987, sequence version 1.

DT 27-JUN-2006, entry version 43.

DE Ig kappa chain V-I region Walker precursor.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Suartchogilres; Primates; Haplorhini;

OC Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RA MEDLINE=85014148; PubMed=6091049;

RA Klobbeck H.G., Combrato G., Zachau H.G.;

RT "Immunoglobulin genes of the kappa light chain type from two human

RT lymphoid cell lines are closely related.";

RL Nucleic Acids Res. 12:6995-7006(1984).

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CC -----

CC EMBL; X00965; CAA32477.1; ALT\_TERM; Genomic\_DNA.

DR PIR; A01883; KLUHWK.

DR HSSP; P01607; 1BWW.

DR SNR; P04431; 23-129.

DR Ensemble1; ENSG00000163245; Homo sapiens.

DR LinkHub; P04431; -.

DR RZPD-ProtExp; IOH14191; -.

DR RZPD-ProtExp; IOH21663; -.

DR RZPD-ProtExp; IOH23035; -.

DR RZPD-ProtExp; IOH23055; -.

DR RZPD-ProtExp; IOH23077; -.

DR RZPD-ProtExp; IOH23168; -.

DR RZPD-ProtExp; IOH23177; -.

DR RZPD-ProtExp; IOH23178; -.

DR RZPD-ProtExp; IOH23179; -.

DR RZPD-ProtExp; IOH29440; -.

DR RZPD-ProtExp; IOH40810; -.

DR RZPD-ProtExp; IOH7177; -.

DR RZPD-ProtExp; T2893; -.

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DR PIR: A90562; K1HUEU.  
DR HSSP; P01607; 1BW.

DR SMR; P01598; 1-107.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig sub.  
DR InterPro; IPR013106; Ig V-set.

DR InterPro; IPR003596; Ig V-set\_sub.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
DR Direct protein sequencing; Immunoglobulin domain;

KW Immunoglobulin V region.  
FT CHAIN 1 >108  
FT REGION 1 23  
FT REGION 24 34  
FT REGION 35 49  
FT REGION 50 56  
FT REGION 57 88  
FT REGION 89 97  
FT REGION 98 107  
FT REGION 98 107  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 80.1%; Score 447; DB 1; Length 108;  
Best Local Similarity 80.4%; Pred. No. 3.6e-38;  
Matches 86; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60  
DB 1 DIQMTQSPSTLSASVGDRTVITTCRASQSIINTLAWYQKPGKAPKRLIMYKASSLESQGVPS 60  
QY 61 RFGSGSGTDTLTITSSLPQDPFATYICLOHNSDPCSPFGQGTKEIR 107  
DB 61 RFGSGSGTETLTITSSLPQDPFATYICQYNSDKMFGQGTKEVK 107

RESULT 13  
KVIV HUMAN STANDARD; PRT; 108 AA.  
AC P04430;  
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.  
DT 13-AUG-1987, sequence version 1.  
DT 30-MAY-2006, entry version 41.  
DE Ig kappa chain V-I region BAN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;  
RA D'wilet F.E., O'Connor T.P., Benson M.D.;  
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";  
RL Mol. Immunol. 23:73-78(1986).

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DR PIR: A01878; K1HUBN.  
DR HSSP; P80362; 1WTL.  
DR SMR; P04430; 1-108.  
DR GO; GO:0005576; C:extracellular region; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig sub.  
DR InterPro; IPR013106; Ig V-set.  
DR InterPro; IPR003596; Ig V-set\_sub.

DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS0835; IG LIKE; 1.  
DR Amyloid; Direct protein sequencing; Immunoglobulin domain;

KW Immunoglobulin V region.  
FT CHAIN 1 >108  
FT REGION 1 23  
FT REGION 24 34  
FT REGION 35 49  
FT REGION 50 56  
FT REGION 57 88  
FT REGION 89 97  
FT REGION 98 107  
FT REGION 98 107  
FT DISULFID 23 88  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.9%; Score 446; DB 1; Length 108;  
Best Local Similarity 79.4%; Pred. No. 4.6e-38;  
Matches 85; Conservative 11; Mismatches 11; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLGYQKPGKAPKRLIYAASSLSQGVPS 60  
DB 1 DIQMTQSPSSLSASVGDRTVITTCRASQSVYVYVAVFQKPGKAPKSLIYDASTLSQGVPS 60  
QY 61 RFGSGSGTDTLTITSSLPQDPFATYICLOHNSDPCSPFGQGTKEIR 107  
DB 61 NFTGSGSGTDTLTITSSLPQDPFATYICQYNSPYTFQGTKEVK 107

RESULT 14  
Q96SA9 HUMAN PRELIMINARY; PRT; 107 AA.  
AC Q96SA9;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 18-APR-2006, entry version 19.  
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain  
DE Variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98375893; PubMed=9712075;  
RA Aderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal monoclonal antibodies from  
RT rheumatic arthritis: human anti-N-acetylglucosamine/anti-myosin  
RT antibody V region genes.";  
RL J. Immunol. 161:2020-2031(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92387224; PubMed=1516616;  
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;  
RT "Human monoclonal striational autoantibodies isolated from thymic B  
RT lymphocytes of patients with myasthenia gravis use VH and VL gene  
RT segments associated with the autoimmune repertoire.";  
RL Eur. J. Immunol. 22:2231-2236(1992).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93170387; PubMed=8436174;  
RA Wagner S.D., Luzzatto L.;  
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are



GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:06:51 ; Search time 13 Seconds  
(without alignments)  
696.311 Million cell updates/sec

Title: US-10-665-383-24

Perfect score: 558

Sequence: 1 DIQWTQSPSSLSASVGRVT.....CLOHNSDPCSFQGTQKLEIR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC Celerra\_SIDS3/prodata/2/iaa/5 COMB.pep.\*
- 2: /EMC Celerra\_SIDS3/prodata/2/iaa/6 COMB.pep.\*
- 3: /EMC Celerra\_SIDS3/prodata/2/iaa/7 COMB.pep.\*
- 4: /EMC Celerra\_SIDS3/prodata/2/iaa/H COMB.pep.\*
- 5: /EMC Celerra\_SIDS3/prodata/2/iaa/PCUS COMB.pep.\*
- 6: /EMC Celerra\_SIDS3/prodata/2/iaa/RE COMB.pep.\*
- 7: /EMC Celerra\_SIDS3/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525	94.1	107	2	US-10-330-613A-18
2	519	93.0	107	2	US-10-330-613A-14
3	490	87.8	107	2	US-09-240-274-29
4	490	87.8	107	2	US-09-848-798-29
5	481	86.2	95	2	US-10-194-975-59
6	481	86.2	95	2	US-10-330-613A-47
7	481	86.2	95	2	US-10-330-613A-48
8	481	86.2	95	2	US-10-330-613A-51
9	481	86.2	95	2	US-10-330-613A-52
10	481	86.2	107	2	US-08-599-226-9
11	481	86.2	107	2	US-09-125-098-9
12	481	86.2	107	2	US-09-540-018-9
13	480	86.0	109	2	US-09-025-769B-28
14	480	86.0	109	2	US-09-025-769B-43
15	480	86.0	109	2	US-09-025-769B-43
16	480	86.0	109	2	US-09-490-070A-28
17	480	86.0	109	2	US-09-490-070A-43
18	480	86.0	109	2	US-09-490-153-28
19	480	86.0	109	2	US-09-490-153-43
20	480	86.0	109	2	US-09-490-324-28
21	479	85.8	107	1	US-07-934-373C-18
22	479	85.8	107	2	US-08-437-642B-18
23	479	85.8	107	2	US-08-146-206C-18
24	479	85.8	107	2	US-09-648-067A-14
25	479	85.8	107	2	US-09-705-686-18
26	479	85.8	107	2	US-09-705-392A-18

27	479	85.8	107	2	US-09-705-398-18
28	479	85.8	107	2	US-09-602-812A-5
29	479	85.8	107	5	PCT-US93-07832-18
30	479	85.8	108	2	US-08-974-899-3
31	479	85.8	108	2	US-09-795-798-3
32	479	85.8	108	2	US-08-908-469-12
33	477	85.5	107	2	US-08-599-226-1
34	477	85.5	107	2	US-09-125-098-1
35	477	85.5	107	2	US-09-540-018-1
36	476	85.3	109	2	US-10-330-613A-10
37	475	85.1	107	2	US-09-644-668A-13
38	474	84.9	108	1	US-08-378-939-32
39	474	84.9	108	1	US-08-378-939-34
40	473	84.8	108	2	US-09-920-262A-8
41	472	84.6	108	1	US-08-378-939-24
42	472	84.6	109	1	US-07-934-373C-3
43	472	84.6	109	2	US-08-437-642B-3
44	472	84.6	109	2	US-08-146-206C-3
45	472	84.6	109	2	US-09-705-686-3

## ALIGNMENTS

### RESULT 1

US-10-330-613A-18  
; Sequence 18, Application US/10330613A  
; Patent No. 6924360  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ARGENTX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613A  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613A-18

Query Match 94.1%; Score 525; DB 2; Length 107;  
Best Local Similarity 94.4%; Pred. No. 8.4e-42;  
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 60

DB 1 DIQWTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 60

QY 61 RFSGSGSGTFTLTISLQPEDFATYTCLOHNSDPCSFQGTQKLEIR 107

DB 61 RFSGSGSGTFTLTISLQPEDFATYTCLOHNSDPCSFQGTQKLEIR 107

### RESULT 2

US-10-330-613A-14  
; Sequence 14, Application US/10330613A  
; Patent No. 6924360  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ARGENTX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613A  
; CURRENT FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 107



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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-14

Query Match      93.0%; Score 519; DB 2; Length 107;
Best Local Similarity 93.5%; Pred. No. 3e-41;
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSLOPEDFATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFGSGSGTEFTLTITSSLOPEDFATYCYCLOHNSVPLTFGGTKVEIK 107

RESULT 3
US-09-240-274-29
; Sequence 29, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain F01
US-09-240-274-29

Query Match      87.8%; Score 490; DB 2; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.5e-38;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 QMTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPSRF 62
Db 2 ELTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPSRF 61

Qy 63 SSGSGGTFDLTITSSLOPEDFATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 62 SSGSGGTEFTLTITSSLOPEDSATYCYCLOHNSFPWTFQGGTKVEIK 106

RESULT 4
US-09-848-798-29
; Sequence 29, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain F01
US-09-240-274-29

Query Match      87.8%; Score 490; DB 2; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.5e-38;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 QMTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPSRF 62
Db 2 ELTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPSRF 61

Qy 63 SSGSGGTFDLTITSSLOPEDFATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 62 SSGSGGTEFTLTITSSLOPEDSATYCYCLOHNSFPWTFQGGTKVEIK 106

RESULT 5
US-10-194-975-59
; Sequence 59, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-59

Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSLOPEDFATYCYCLOHNSDP 95
Db 61 RFGSGSGTEFTLTITSSLOPEDFATYCYCLOHNSYP 95

RESULT 6
US-10-330-613A-47
; Sequence 47, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-47

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; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain F01
US-09-848-798-29

Query Match      87.8%; Score 490; DB 2; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.5e-38;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 QMTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPSRF 62
Db 2 ELTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPSRF 61

Qy 63 SSGSGGTFDLTITSSLOPEDFATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 62 SSGSGGTEFTLTITSSLOPEDSATYCYCLOHNSFPWTFQGGTKVEIK 106

RESULT 5
US-10-194-975-59
; Sequence 59, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-59

Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSLOPEDFATYCYCLOHNSDP 95
Db 61 RFGSGSGTEFTLTITSSLOPEDFATYCYCLOHNSYP 95

RESULT 6
US-10-330-613A-47
; Sequence 47, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-47

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Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTFTLTISSLQPEDFATYYCLOHNSDP 95
Db 61 RFSGSGGTFTLTISSLQPEDFATYYCLOHNSYP 95

RESULT 7
US-10-330-613A-48
; Sequence 48, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-48

Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTFTLTISSLQPEDFATYYCLOHNSDP 95
Db 61 RFSGSGGTFTLTISSLQPEDFATYYCLOHNSYP 95

RESULT 8
US-10-330-613A-51
; Sequence 51, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-51

Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
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Qy 61 RFSGSGGTFTLTISSLQPEDFATYYCLOHNSDP 95
Db 61 RFSGSGGTFTLTISSLQPEDFATYYCLOHNSYP 95

RESULT 9
US-10-330-613A-52
; Sequence 52, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-52

Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTFTLTISSLQPEDFATYYCLOHNSDP 95
Db 61 RFSGSGGTFTLTISSLQPEDFATYYCLOHNSYP 95

RESULT 10
US-08-599-226-9
; Sequence 9, Application US/08599226
; Patent No. 6090382
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
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; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
;
US-09-125-098-9

Query Match 86.2%; Score 481; DB 2; Length 107;
Best Local Similarity 86.9%; Pred. No. 1.1e-37;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTITTCRASGIRNDLIGWYQKPGKAPKRLIYAASSIQSGVPS 60
DB 1 DIQMTQSPSSLSASIGDRTITTCRASGIRNLYAWYQKPGKAPKLLIYAASTLQSGVPS 60

QY 61 RFSGSGSGTDFTLTITSLQPEDPATYICLQHNSDPCSFQGGTKLEIR 107
DB 61 RFSGSGSGTDFTLTITSLQPEDVATYYCQKYNAPYAFGGTKVEIK 107

RESULT 12
US-09-540-018-9
; Sequence 9, Application US/09540018
; Patent No. 6509015
; GENERAL INFORMATION:
; APPLICANT: Salfield, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFA
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/540,018
; FILING DATE: 31-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
; FILING DATE: 08-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-540-018-9

Query Match      86.2%; Score 481; DB 2; Length 107;
Best Local Similarity 86.9%; Pred. No. 1.1e-37;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISSLQPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDFTLTISSLQPEDFATYYCLOHNSDPCSFQGTKEIR 107

RESULT 13
US-09-025-769B-28
; Sequence 28, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-28

Query Match      86.0%; Score 480; DB 2; Length 109;
Best Local Similarity 87.9%; Pred. No. 1.3e-37;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISSLQPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDFTLTISSLQPEDFATYYCLOHNSDPCSFQGTKEIR 107

RESULT 14
US-09-025-769B-43
; Sequence 43, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-43

Query Match      85.0%; Score 480; DB 2; Length 109;
Best Local Similarity 87.9%; Pred. No. 1.3e-37;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISSLQPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDFTLTISSLQPEDFATYYCLOHNSDPCSFQGTKEIR 107

RESULT 15
US-09-490-070A-28
; Sequence 28, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
```

```

Pack, Peter
Ilag, Vic
Ge. Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSES: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: US/09/490,070A
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-490-070A-28

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Query Match      86.0%; Score 480; DB 2; Length 109;
Best Local Similarity 87.9%; Pred. No. 1.3e-37;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQPSLSASVGDRTVITCRASQGIKNDLWYQKPKAPKLLIYAASLSQGVPS 60
   |||||
Db 1 DIQMTQPSLSASVGDRTVITCRASQGISSYLAWYQKPKAPKLLIYAASLSQGVPS 60
   |||||

QY 61 RFGSGSGTDFTLTISLQPEDFATYYCLOHNSDPCSFQGGTKLEIR 107
   |||||
Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQGHYTPPTFGGTVK 107
   |||||

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Search completed: April 25, 2007, 04:08:29  
Job time : 14.4506 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 40 Seconds  
(without alignments)  
1251.741 Million cell updates/sec

Title: US-10-665-383-24

Perfect score: 558

Sequence: 1 DIQMTSPSLASVGRVT.....CLQHNSDPCSFQGTKEIR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	107	4	US-10-041-860-22
2	558	100.0	107	4	US-10-041-860-227
3	558	100.0	107	4	US-10-041-860-261
4	558	100.0	107	4	US-10-041-860-262
5	558	100.0	107	4	US-10-041-860-297
6	558	100.0	107	4	US-10-665-383-24
7	542	97.1	107	4	US-10-684-109-53
8	542	97.1	234	4	US-10-684-109-109
9	539	96.6	107	4	US-10-684-109-41
10	539	96.6	234	4	US-10-684-109-91
11	528	94.6	107	4	US-10-041-860-265
12	528	94.6	236	4	US-10-038-591-48
13	528	94.6	236	4	US-10-775-444A-48
14	528	94.6	236	6	US-11-144-248-48
15	528	94.6	236	6	US-11-144-223-48
16	528	94.6	236	6	US-11-182-343-48
17	527	94.4	108	5	US-10-805-177-68
18	527	94.4	108	5	US-10-805-177-72
19	525	94.1	107	4	US-10-330-613-18
20	525	94.1	107	4	US-10-330-530-18
21	525	94.1	107	4	US-10-041-860-26
22	525	94.1	107	4	US-10-041-860-28
23	525	94.1	107	4	US-10-041-860-36
24	525	94.1	107	4	US-10-041-860-231
25	525	94.1	107	4	US-10-041-860-232
26	525	94.1	107	4	US-10-041-860-234
27	525	94.1	107	4	US-10-041-860-266

## ALIGNMENTS

### RESULT 1

US-10-041-860-22  
; Sequence 22, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: ARGENIX.051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-22

Query Match 100.0%; Score 558; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.3e-40;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIQMTSPSLASVGRVTITCRASQGINDLGWYQKPKAPKRLIYAASSLSQSGVPS	60
DB	1	DIQMTSPSLASVGRVTITCRASQGINDLGWYQKPKAPKRLIYAASSLSQSGVPS	60
QY	61	RFGSGSGTDTTITISSLPEDPATYTCLOHNSDPCSFQGTKEIR	107
DB	61	RFGSGSGTDTTITISSLPEDPATYTCLOHNSDPCSFQGTKEIR	107

### RESULT 2

US-10-041-860-227  
; Sequence 227, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi

28	525	94.1	107	4	US-10-041-860-268	Sequence 268, App
29	525	94.1	107	4	US-10-041-860-316	Sequence 316, App
30	525	94.1	107	4	US-10-041-860-340	Sequence 340, App
31	525	94.1	107	4	US-10-309-762-166	Sequence 166, App
32	525	94.1	107	4	US-10-660-357-18	Sequence 18, App
33	525	94.1	107	4	US-10-665-383-32	Sequence 32, App
34	525	94.1	107	4	US-10-665-383-36	Sequence 36, App
35	525	94.1	107	4	US-10-665-383-52	Sequence 52, App
36	525	94.1	107	5	US-10-727-155-274	Sequence 274, App
37	525	94.1	107	5	US-10-727-155-307	Sequence 307, App
38	525	94.1	236	4	US-10-038-591-52	Sequence 52, App
39	525	94.1	236	4	US-10-775-444A-52	Sequence 52, App
40	525	94.1	236	5	US-10-917-073A-6	Sequence 6, App
41	525	94.1	236	6	US-11-144-248-52	Sequence 52, App
42	525	94.1	236	6	US-11-144-222-52	Sequence 52, App
43	525	94.1	236	6	US-11-182-343-52	Sequence 52, App
44	524	93.9	107	5	US-10-727-155-60	Sequence 60, App
45	524	93.9	107	5	US-10-822-306A-16	Sequence 16, App

```
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 227
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-227

Query Match          100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 3
US-10-041-860-261
; Sequence 261, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE OF INVENTION: THEREOF
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-261

Query Match          100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 4
US-10-041-860-262
; Sequence 262, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
```

```
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-262

Query Match          100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 5
US-10-041-860-297
; Sequence 297, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-297

Query Match          100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 6
US-10-041-860-297
; Sequence 297, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-297

Query Match          100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPKGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
```

```

US-10-665-383-24
; Sequence 24, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: Laroche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; PRIOR FILING DATE: 2003-09-16
; PRIOR FILING DATE: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-24

Query Match      100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 107
Db 61 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 107

RESULT 7
US-10-684-109-53
; Sequence 53, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR FILING DATE: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-53

Query Match      97.1%; Score 542; DB 4; Length 107;
Best Local Similarity 97.2%; Pred. No. 3.1e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 107
Db 61 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 107

RESULT 8
US-10-684-109-109
; Sequence 109, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR FILING DATE: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-109

Query Match      97.1%; Score 542; DB 4; Length 234;
Best Local Similarity 97.2%; Pred. No. 6.5e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 21 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 80

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 107
Db 81 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 127

RESULT 9
US-10-684-109-41
; Sequence 41, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR FILING DATE: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-41

Query Match      96.6%; Score 539; DB 4; Length 107;
Best Local Similarity 96.3%; Pred. No. 5.5e-39;
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60

```





61 RFSGSGGTDFTLTISSLQPEDFATYICLQHNSDPCSFQGTKEIR 107  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 83 RFSGSGGTEFTLTISLQPEDFATYICLQHNSYPYTFQGTKEIK 129



```

; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 227
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-227

Query Match 100.0%; Score 558; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107

RESULT 3
US-11-109-181-261
; Sequence 261, Application US/11/109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-261

Query Match 100.0%; Score 558; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107

RESULT 4
US-11-109-181-262
; Sequence 262, Application US/11/109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-262

Query Match 100.0%; Score 558; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107

RESULT 5
US-11-109-181-297
; Sequence 297, Application US/11/109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-297

Query Match 100.0%; Score 558; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107
```

```
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGTKEIR 107

RESULT 6
US-11-433-924-384
; Sequence 384, Application US/11433924
; Publication No. US20060286112A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Aimee
; APPLICANT: Foord, Orit
; APPLICANT: Belouski, Shelley Sims
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
; TITLE OF INVENTION: OTHER DISORDERS
; FILE REFERENCE: ABGENIX.120A
; CURRENT APPLICATION NUMBER: US/11/433,924
; CURRENT FILING DATE: 2006-05-12
; PRIOR APPLICATION NUMBER: US 60/681,846
; PRIOR FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 384
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-433-924-384

Query Match 97.1%; Score 542; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 4.6e-43;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGTKEIR 107

RESULT 7
US-11-433-924-376
; Sequence 376, Application US/11433924
; Publication No. US20060286112A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Aimee
; APPLICANT: Foord, Orit
; APPLICANT: Belouski, Shelley Sims
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
; TITLE OF INVENTION: OTHER DISORDERS
; FILE REFERENCE: ABGENIX.120A
; CURRENT APPLICATION NUMBER: US/11/433,924
; CURRENT FILING DATE: 2006-05-12
; PRIOR APPLICATION NUMBER: US 60/681,846
; PRIOR FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-433-924-376
```

```
Query Match 95.9%; Score 535; DB 7; Length 107;
Best Local Similarity 95.3%; Pred. No. 2.1e-42;
Matches 102; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGTKEIR 107

RESULT 8
US-11-109-181-265
; Sequence 265, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R. F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-265

Query Match 94.6%; Score 528; DB 7; Length 107;
Best Local Similarity 95.3%; Pred. No. 9.2e-42;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDTFTLTISLQPEDPATYCYCLOHNSDPCSFQGTKEIR 107

RESULT 9
US-10-515-149-39
; Sequence 39, Application US/10515149
; Publication No. US20060194276A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna
; APPLICANT: Krauss, Juergen
; APPLICANT: Arndt, Michaela
; APPLICANT: Martin, Andrew C. R.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: University of Reading
; TITLE OF INVENTION: Specificity Framework
; TITLE OF INVENTION: Framework
; FILE REFERENCE: 015280-459100US
; CURRENT APPLICATION NUMBER: US/10/515,149
; CURRENT FILING DATE: 2004-11-18
```

; PRIOR APPLICATION NUMBER: US 60/390,033  
; PRIOR FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: WO PCT/US03/19333  
; PRIOR FILING DATE: 2003-06-17  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human V-L germline sequence  
US-10-515-149-39

Query Match 94.6%; Score 528; DB 6; Length 108;  
Best Local Similarity 95.3%; Pred. No. 9.3e-42;  
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASLSQGVPS 60  
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASLSQGVPS 60  
QY 61 RPSGSGGTDFLTITSSLOPEDPATYCYCLQHNSDPCSFQGTKEIR 107  
Db 61 RPSGSGGTDFLTITSSLOPEDPATYCYCLQHNSDPCSFQGTKEIR 107

RESULT 10  
US-11-346-403A-61  
; Sequence 61, Application US/11346403A  
; Publication No. US20060234302A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoet, Rene  
; APPLICANT: Schoonbroodt, Sonia  
; APPLICANT: Ladner, Robert C.  
; TITLE OF INVENTION: LIBRARIES AND METHODS FOR  
; TITLE OF INVENTION: ISOLATING ANTIBODIES  
; FILE REFERENCE: 10280-116001  
; CURRENT APPLICATION NUMBER: US/11/346,403A  
; CURRENT FILING DATE: 2006-02-01  
; PRIOR APPLICATION NUMBER: US 60/649,065  
; PRIOR FILING DATE: 2005-02-01  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
US-11-346-403A-61

Query Match 94.6%; Score 528; DB 7; Length 108;  
Best Local Similarity 95.3%; Pred. No. 9.3e-42;  
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASLSQGVPS 60  
Db 2 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASLSQGVPS 61  
QY 61 RPSGSGGTDFLTITSSLOPEDPATYCYCLQHNSDPCSFQGTKEIR 107  
Db 62 RPSGSGGTDFLTITSSLOPEDPATYCYCLQHNSDPCSFQGTKEIR 108

RESULT 11  
US-11-290-687-27  
; Sequence 27, Application US/11290687  
; Publication No. US20060140960A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Yan  
; APPLICANT: Pachter, Jonathan  
; APPLICANT: Wang, Yaolin

; APPLICANT: Liu, Ming  
; TITLE OF INVENTION: BIOMARKERS FOR PRE-SELECTION OF PATIENTS FOR ANTI-IGF1R THERAPY  
; FILE REFERENCE: JB06257 US01  
; CURRENT APPLICATION NUMBER: US/11/290,687  
; CURRENT FILING DATE: 2005-11-30  
; PRIOR APPLICATION NUMBER: 60/633,156  
; PRIOR FILING DATE: 2004-12-03  
; NUMBER OF SEQ ID NOS: 105  
; SOFTWARE: Patent In version 3.3  
; SEQ ID NO 27  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: light chain immunoglobulin  
US-11-290-687-27

Query Match 94.6%; Score 528; DB 7; Length 236;  
Best Local Similarity 95.3%; Pred. No. 2.1e-41;  
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASLSQGVPS 60  
Db 23 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASLSQGVPS 82  
QY 61 RPSGSGGTDFLTITSSLOPEDPATYCYCLQHNSDPCSFQGTKEIR 107  
Db 83 RPSGSGGTDFLTITSSLOPEDPATYCYCLQHNSDPCSFQGTKEIR 129

RESULT 12  
US-11-404-967-27  
; Sequence 27, Application US/11404967  
; Publication No. US20060233810A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Yaolin  
; APPLICANT: Liu, Ming  
; APPLICANT: Wang, Yan  
; APPLICANT: Pachter, Jonathan A  
; APPLICANT: Bishop, Walter R  
; TITLE OF INVENTION: Methods and Compositions for Treating or Preventing Cancer  
; FILE REFERENCE: OC06331 US  
; CURRENT APPLICATION NUMBER: US/11/404,967  
; CURRENT FILING DATE: 2006-04-14  
; PRIOR APPLICATION NUMBER: 60/671,654  
; PRIOR FILING DATE: 2005-04-15  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patent In version 3.3  
; SEQ ID NO 27  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: light chain immunoglobulin  
US-11-404-967-27

Query Match 94.6%; Score 528; DB 7; Length 236;  
Best Local Similarity 95.3%; Pred. No. 2.1e-41;  
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASLSQGVPS 60  
Db 23 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASLSQGVPS 82  
QY 61 RPSGSGGTDFLTITSSLOPEDPATYCYCLQHNSDPCSFQGTKEIR 107  
Db 83 RPSGSGGTDFLTITSSLOPEDPATYCYCLQHNSDPCSFQGTKEIR 129

RESULT 13  
US-11-239-308-8  
; Sequence 8, Application US/11239308  
; Publication No. US20060088883A1

```

; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR FILING DATE: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-8

Query Match          94.1%; Score 525; DB 7; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.8e-41;
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISSLPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDFTLTISSLPEDFATYYCLOHNSYPWTFGQGTKEIK 107

RESULT 14
US-11-479-339-18
; Sequence 18, Application US/11/479339
; Publication No. US20060246077A1
; GENERAL INFORMATION:
; APPLICANT: Menashe, Bar-El
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ARGENIX 030C2
; CURRENT APPLICATION NUMBER: US/11/479,339
; CURRENT FILING DATE: 2006-06-30
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346,460
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-479-339-18

Query Match          94.1%; Score 525; DB 7; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.8e-41;
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISSLPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDFTLTISSLPEDFATYYCLOHNSYPWTFGQGTKEIK 107

RESULT 15
US-11-109-181-26
; Sequence 26, Application US/11/109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX 051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-26

Query Match          94.1%; Score 525; DB 7; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.8e-41;
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFTLTISSLPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDFTLTISSLPEDFATYYCLOHNSYPWTFGQGTKEIK 107

Search completed: April 25, 2007, 04:27:43
Job time : 41.2585 secs
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GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 112 Seconds  
(without alignments)  
564.248 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EYLVQSGAEVKKPGESLKI.....YYHGMVDWVGQGTIVTSS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_200701:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*  
10: Geneseqp2006s:\*  
11: Geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	699	100.0	129	7	ADK18605
2	699	100.0	129	7	ADK18791
3	699	100.0	129	7	ADK18895
4	699	100.0	129	7	ADK18826
5	699	100.0	129	8	ADL25428
6	623	89.1	474	9	AEA12652
7	623	89.1	474	9	AEA12653
8	623	89.1	474	9	AEA18909
9	623	89.1	474	9	AEA18908
10	623	89.1	474	9	AEA18548
11	623	89.1	474	9	AEA18549
12	623	89.1	474	9	AEA10642
13	623	89.1	474	9	AEA10641
14	623	89.1	474	9	AEA10641
15	623	89.1	474	9	AEA10641
16	623	89.1	474	9	AEA10641
17	623	89.1	474	9	AEA10641
18	623	89.1	474	9	AEA10641
19	623	89.1	474	9	AEA10641
20	603	86.3	125	9	ADY26764
21	598.5	85.6	126	7	ADK18889
22	593.5	84.9	126	7	ADK18603

23	593.5	84.9	126	7	ADK18790	Adk18790 Anti-huma
24	593.5	84.9	126	7	ADK18825	Adk18825 Anti-huma
25	593.5	84.9	126	8	ADL25424	Adl25424 Human mAb
26	592.5	84.8	126	7	ADK18876	Adk18876 Anti-huma
27	592.5	84.8	126	7	ADK18599	Adk18599 Anti-huma
28	592.5	84.8	126	7	ADK18824	Adk18824 Anti-huma
29	592.5	84.8	126	8	ADL25416	Adl25416 Human mAb
30	592	84.7	156	10	AEK98291	Aek98291 Human 161
31	592	84.7	156	10	AEK98296	Aek98296 Human 161
32	592	84.7	182	10	AEK98221	Aek98221 Human 161
33	592	84.7	182	10	AEK98278	Aek98278 Human 161
34	590	84.4	118	8	ADP47228	Adp47228 Human pho
35	590	84.4	178	10	AEK98274	Aek98274 Human 161
36	590	84.4	178	10	AEK98213	Aek98213 Human 161
37	589.5	84.3	126	7	ADK18827	Adk18827 Anti-huma
38	589.5	84.3	126	7	ADK18611	Adk18611 Anti-huma
39	589.5	84.3	126	7	ADK18792	Adk18792 Anti-huma
40	589.5	84.3	126	7	ADK18913	Adk18913 Anti-huma
41	589.5	84.3	126	8	ADL25440	Adl25440 Human mAb
42	587	84.0	118	8	ADP47088	Adp47088 Human pho
43	595	83.7	118	8	ADP47224	Adp47224 Human pho
44	584	83.5	118	8	ADP47225	Adp47225 Human pho
45	584	83.5	118	8	ADP47098	Adp47098 Human pho

#### ALIGNMENTS

##### RESULT 1

ADK18605

ID ADK18605 standard; protein; 129 AA.

AC ADK18605;

DT 06-MAY-2004 (first entry)

DE Anti-human PDGF-D antibody heavy chain protein sequence.

XW antiinflammatory; immunomodulator; cytostatic; gene therapy.

OS Homo sapiens.

PN WO2003057857-A2.

PD 17-JUL-2003.

PF 06-JAN-2003; 2003WO-US000398.

PR 07-JAN-2002; 2002US-00041860.

PA (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;

XX Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

PS Disclosure; SEQ ID NO 29; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

```
XX SQ Sequence 129 AA;
Query Match 100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGVWRQMPGKGLWMMGIIYPGDSSTRY 60
DB 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGVWRQMPGKGLWMMGIIYPGDSSTRY 60

QY 61 SPSPFQQTATISADKSIATAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120
DB 61 SPSPFQQTATISADKSIATAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120

QY 121 QGTTVTVSS 129
DB 121 QGTTVTVSS 129

RESULT 2
ADK18791
ID ADK18791 standard; protein; 129 AA.
AC ADK18791;
XX
XX 06-MAY-2004 (first entry)
XX
XX Anti-human PDGF-D antibody protein related sequence #17.
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX Homo sapiens.
XX WO2003057857-A2.
XX 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX 07-JAN-2002; 2002US-00041860.
XX (ABGE-) ABGENIX INC.
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 215; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 129 AA;
Query Match 100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGVWRQMPGKGLWMMGIIYPGDSSTRY 60
```

```
DB 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGVWRQMPGKGLWMMGIIYPGDSSTRY 60
QY 61 SPSPFQQTATISADKSIATAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120
DB 61 SPSPFQQTATISADKSIATAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120

QY 121 QGTTVTVSS 129
DB 121 QGTTVTVSS 129

RESULT 3
ADK18895
ID ADK18895 standard; protein; 129 AA.
XX
XX AC ADK18895;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Anti-human PDGF-D antibody protein related sequence #121.
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX KW
XX OS Homo sapiens.
XX PN WO2003057857-A2.
XX
XX PD 17-JUL-2003.
XX
XX PF 06-JAN-2003; 2003WO-US000398.
XX
XX PR 07-JAN-2002; 2002US-00041860.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 319; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 129 AA;
Query Match 100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGVWRQMPGKGLWMMGIIYPGDSSTRY 60
DB 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGVWRQMPGKGLWMMGIIYPGDSSTRY 60

QY 61 SPSPFQQTATISADKSIATAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120
DB 61 SPSPFQQTATISADKSIATAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120

QY 121 QGTTVTVSS 129
```



```

Db      121 QGTTVTSS 129
|||||
RESULT 4
ADK18826
ID ADK18826 standard; protein; 129 AA.
XX
AC ADK18826;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody protein related sequence #52.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 250; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
SQ Sequence 129 AA;

Query Match      100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPQESLKISKKGSGYFTSYWIGVRQMPGKGLWNGIYPGDSSTRY 60
Db 1 EVQLVQSGAEVKKPQESLKISKKGSGYFTSYWIGVRQMPGKGLWNGIYPGDSSTRY 60
QY 61 SPSPGQATISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120
Db 61 SPSPGQATISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120
QY 121 QGTTVTSS 129
Db 121 QGTTVTSS 129

RESULT 5
ADL25428
ID ADL25428 standard; protein; 129 AA.
XX
AC ADL25428;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human mAb 1.29 heavy chain variable region protein SEQ ID NO:38.
XX
KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW nephritis; mesangial cell proliferation inhibition;
KW mesangial proliferative glomerulonephritis; nephrotropic;
KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW gene therapy; human; monoclonal antibody; mAb.
XX
OS Homo sapiens.
XX
PN WO2004024098-A2.
XX
PD 25-MAR-2004.
XX
PF 16-SEP-2003; 2003WO-US029414.
XX
PR 16-SEP-2002; 2002US-0411137P.
XX
PA (ABGE-) ABGENIX INC.
PA (CURA-) CURAGEN CORP.
XX
PI Floege J, Gazit-Bornstein G, Keyt B, Larochelle WJ, Lichenstein H;
PI WPI; 2004-269881/25.
DR N-PSDB; ADL25427.
XX
PT Use of an antibody or its binding fragment that binds platelet derived
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT nephritis.
XX
PS Disclosure; SEQ ID NO 38; 115pp; English.
XX
CC The present invention describes an antibody or its binding fragment that
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC useful in preparing a medicament for treating nephritis. Also described:
CC (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC of treating mesangial proliferative glomerulonephritis. The antibody has
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC antidiabetic activities, and can be used in gene therapy. The antibody or
CC its binding fragment, that binds PDGF-DD, can be used in preparing a
CC medicament for treating nephritis and related disorders, e.g., mesangial
CC proliferative glomerulonephritis. The present sequence represents a human
CC monoclonal antibody (mAb) variable region sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 129 AA;

Query Match      100.0%; Score 699; DB 8; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPQESLKISKKGSGYFTSYWIGVRQMPGKGLWNGIYPGDSSTRY 60
Db 1 EVQLVQSGAEVKKPQESLKISKKGSGYFTSYWIGVRQMPGKGLWNGIYPGDSSTRY 60
QY 61 SPSPGQATISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120
Db 61 SPSPGQATISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120
QY 121 QGTTVTSS 129
Db 121 QGTTVTSS 129

RESULT 6
AEA12652
ID AEA12652 standard; protein; 474 AA.
XX

```

AC AEA12652;  
 XX 28-JUL-2005 (first entry)  
 XX Heavy chain of CHIR-5.9 human anti-CD40 antibody.  
 DE cancer; B-cell; antibody therapy; CD40; CD20; tumor; cytostatic;  
 KW b-cell acute lymphoblastic leukemia; b-cell lymphoma; heavy chain.  
 XX Homo sapiens.  
 OS  
 XX WO2005044307-A2.  
 PN  
 XX 19-MAY-2005.  
 PD  
 XX 04-NOV-2004; 2004WO-US037159.  
 PF  
 XX 04-NOV-2003; 2003US-0517337P.  
 PR  
 XX 26-NOV-2003; 2003US-0525579P.  
 PR  
 XX 27-APR-2004; 2004US-0565710P.  
 PR  
 XX 28-SEP-2004; 2004US-0613885P.  
 PR  
 XX (CHIR ) CHIRON CORP.  
 PA  
 XX Long L, Luqman M, Yabannavar A, Zaror I;  
 PI  
 XX WPI; 2005-346957/35.  
 XX  
 XX Treating human subjects for B cell-related cancers (e.g. multiple myeloma  
 PT of Burkitt's lymphoma) comprises administering to the subject an amount  
 PT of an antagonist anti-CD40 antibody in combination with an anti-CD20  
 PT antibody.  
 XX  
 XX Claim 1; SEQ ID NO 7; 133pp; English.  
 PS  
 XX The invention relates to a novel method for treating a human subject for  
 CC a cancer characterized by neoplastic B cell growth. The method comprises  
 CC administering to the subject combination antibody therapy, which  
 CC comprises an amount of an anti-CD40 antibody or its antigen-binding  
 CC fragment in combination with an anti-CD20 antibody or its antigen-binding  
 CC fragment, where the anti-CD40 antibody or antigen-binding fragment is  
 CC free of significant agonist activity when bound to the CD40 antigen. The  
 CC invention further comprises; methods of inhibiting the growth of a tumor  
 CC comprising neoplastic B cells. The methods and compositions have  
 CC cytostatic activity. The methods are useful for treating B cell-related  
 CC cancer (e.g. lymphoma or leukemia) or in manufacturing medicaments for  
 CC the treatment of such a disease. This sequence represents a heavy chain  
 CC of CHIR-5.9 human anti-CD40 antibody of the invention.  
 XX  
 XX Sequence 474 AA;  
 SQ  
 Query Match 89.1%; Score 623; DB 9; Length 474;  
 Best Local Similarity 91.5%; Pred. NO. 1.8e-48;  
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;  
 QY 1 EVQLVQSGAEVKKPESLKISKCSGYSFTSWIGVWRMPGKGLWNGIYPGDSSTRY 60  
 DB 20 EVQLVQSGAEVKKPESLKISKCSGYSFTSWIGVWRMPGKGLWNGIYPGDSSTRY 79  
 QY 61 SPSPGQATISADKSTAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120  
 DB 80 SPSPGQVTTISADKSTAYLQWSSLKASDTAMYCAR----GTAAGRDYHYHYHGMVDVWG 135  
 QY 121 QGTTVTSS 129  
 DB 136 QGTTVTSS 144  
 RESULT 7  
 AEA12653  
 ID AEA12653 standard; protein; 474 AA.  
 XX  
 AC AEA12653;

XX 28-JUL-2005 (first entry)  
 XX Heavy chain variant of CHIR-5.9 human anti-CD40 antibody.  
 DE cancer; B-cell; antibody therapy; CD40; CD20; tumor; cytostatic;  
 KW b-cell acute lymphoblastic leukemia; b-cell lymphoma; heavy chain;  
 KW munitin.  
 XX Homo sapiens.  
 OS  
 OS Synthetic.  
 XX WO2005044307-A2.  
 PN  
 XX 19-MAY-2005.  
 PD  
 XX 04-NOV-2004; 2004WO-US037159.  
 PF  
 XX 04-NOV-2003; 2003US-0517337P.  
 PR  
 XX 26-NOV-2003; 2003US-0525579P.  
 PR  
 XX 27-APR-2004; 2004US-0565710P.  
 PR  
 XX 28-SEP-2004; 2004US-0613885P.  
 PR  
 XX (CHIR ) CHIRON CORP.  
 PA  
 XX Long L, Luqman M, Yabannavar A, Zaror I;  
 PI  
 XX WPI; 2005-346957/35.  
 XX  
 XX Treating human subjects for B cell-related cancers (e.g. multiple myeloma  
 PT of Burkitt's lymphoma) comprises administering to the subject an amount  
 PT of an antagonist anti-CD40 antibody in combination with an anti-CD20  
 PT antibody.  
 XX  
 XX Claim 1; SEQ ID NO 8; 133pp; English.  
 PS  
 XX The invention relates to a novel method for treating a human subject for  
 CC a cancer characterized by neoplastic B cell growth. The method comprises  
 CC administering to the subject combination antibody therapy, which  
 CC comprises an amount of an anti-CD40 antibody or its antigen-binding  
 CC fragment in combination with an anti-CD20 antibody or its antigen-binding  
 CC fragment, where the anti-CD40 antibody or antigen-binding fragment is  
 CC free of significant agonist activity when bound to the CD40 antigen. The  
 CC invention further comprises; methods of inhibiting the growth of a tumor  
 CC comprising neoplastic B cells. The methods and compositions have  
 CC cytostatic activity. The methods are useful for treating B cell-related  
 CC cancer (e.g. lymphoma or leukemia) or in manufacturing medicaments for  
 CC the treatment of such a disease. This sequence represents a heavy chain  
 CC variant of a CHIR-5.9 human anti-CD40 antibody of the invention.  
 XX  
 XX Sequence 474 AA;  
 SQ  
 Query Match 89.1%; Score 623; DB 9; Length 474;  
 Best Local Similarity 91.5%; Pred. NO. 1.8e-48;  
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;  
 QY 1 EVQLVQSGAEVKKPESLKISKCSGYSFTSWIGVWRMPGKGLWNGIYPGDSSTRY 60  
 DB 20 EVQLVQSGAEVKKPESLKISKCSGYSFTSWIGVWRMPGKGLWNGIYPGDSSTRY 79  
 QY 61 SPSPGQATISADKSTAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120  
 DB 80 SPSPGQVTTISADKSTAYLQWSSLKASDTAMYCAR----GTAAGRDYHYHYHGMVDVWG 135  
 QY 121 QGTTVTSS 129  
 DB 136 QGTTVTSS 144  
 RESULT 8  
 AEA18909  
 ID AEA18909 standard; protein; 474 AA.  
 XX

```

AC AEA18909;
XX
DT 28-JUL-2005 (first entry)
XX
DE Variant heavy chain of CHIR-5.9 human anti-CD40 antibody.
XX
DE chronic lymphocytic leukemia; CLL; anti-CD40 antibody; CD40; CHIR-5.9;
XX
DE CHIR-12.12; antibody therapy; heavy chain.
XX
XX Synthetic.
XX
OS Key Location/Qualifiers
XX FH 1. .19
XX FT Peptide /note= "leader peptide"
XX FT 20. .144
XX FT Region /note= "variable region"
XX FT 145. .474
XX FT Region /note= "constant region"
XX
XX WO2005044304-A2.
XX
XX 19-MAY-2005.
XX
XX 04-NOV-2004; 2004WO-US036954.
XX
XX 04-NOV-2003; 2003US-0517337P.
XX
XX 26-NOV-2003; 2003US-0525579P.
XX
XX 27-APR-2004; 2004US-0565710P.
XX
XX 21-SEP-2004; 2004US-0611794P.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Long L, Luqman M, Yabannavar A, Zaror I, Aukerman L;
XX
XX WPI; 2005-346955/35.
XX
XX Treating human subjects for chronic lymphocytic leukemia comprises
XX administering to the subject an amount of a human antagonist anti-CD40
XX monoclonal antibody that specifically binds to the CD40 antigen.
XX
XX Claim 1; SEQ ID NO 8; 115pp; English.
XX
XX The specification describes a method of treating a human subject for
XX chronic lymphocytic leukemia (CLL). The method comprises administering an
XX amount of a human anti-CD40 monoclonal antibody that specifically binds
XX to a human CD40 antigen expressed on the surface of a human CD40-
XX expressing cell and is free of significant agonist activity, where when
XX the antibody binds to the CD40 antigen expressed on the surface of the
XX cell, the growth or differentiation of the cell is inhibited. The human
XX anti-CD40 monoclonal antibody is selected from CHIR-5.9 or CHIR-12.12.
XX The method of the invention is useful for treating chronic lymphocytic
XX leukemia or in manufacturing medicaments for the treatment of such
XX diseases. The present sequence represents a variant heavy chain of human
XX anti-CD40 monoclonal antibody CHIR-5.9.
XX
SQ Sequence 474 AA;
Query Match 89.1%; Score 623; DB 9; Length 474;
Best Local Similarity 91.5%; Pred. No. 1.8e-48;
Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
QY 1 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVROMPGKLEWMIYPGSDTRY 60
DB 20 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVROMPGKLEWMIYPGSDTRY 79
QY 61 SPSFQQTATISADKSIISTAYLQWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVWG 120
DB 80 SPSFQQTATISADKSIISTAYLQWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVWG 135
QY 121 QGTTVTSS 129
DB 136 QGTTVTSS 144
RESULT 9
AEA18908
ID AEA18908 standard; protein; 474 AA.
XX
XX AEA18908;
XX
XX 28-JUL-2005 (first entry)
DT

```

```

XX
DE Heavy chain of CHIR-5.9 human anti-CD40 antibody.
XX
XX chronic lymphocytic leukemia; CLL; anti-CD40 antibody; CD40; CHIR-5.9;
XX
XX CHIR-12.12; antibody therapy; heavy chain.
XX
XX Synthetic.
XX
OS Key Location/Qualifiers
XX FH 1. .19
XX FT Peptide /note= "leader peptide"
XX FT 20. .144
XX FT Region /note= "variable region"
XX FT 145. .474
XX FT Region /note= "constant region"
XX
XX WO2005044304-A2.
XX
XX 19-MAY-2005.
XX
XX 04-NOV-2004; 2004WO-US036954.
XX
XX 04-NOV-2003; 2003US-0517337P.
XX
XX 26-NOV-2003; 2003US-0525579P.
XX
XX 27-APR-2004; 2004US-0565710P.
XX
XX 21-SEP-2004; 2004US-0611794P.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Long L, Luqman M, Yabannavar A, Zaror I, Aukerman L;
XX
XX WPI; 2005-346955/35.
XX
XX Treating human subjects for chronic lymphocytic leukemia comprises
XX administering to the subject an amount of a human antagonist anti-CD40
XX monoclonal antibody that specifically binds to the CD40 antigen.
XX
XX Claim 1; SEQ ID NO 7; 115pp; English.
XX
XX The specification describes a method of treating a human subject for
XX chronic lymphocytic leukemia (CLL). The method comprises administering an
XX amount of a human anti-CD40 monoclonal antibody that specifically binds
XX to a human CD40 antigen expressed on the surface of a human CD40-
XX expressing cell and is free of significant agonist activity, where when
XX the antibody binds to the CD40 antigen expressed on the surface of the
XX cell, the growth or differentiation of the cell is inhibited. The human
XX anti-CD40 monoclonal antibody is selected from CHIR-5.9 or CHIR-12.12.
XX The method of the invention is useful for treating chronic lymphocytic
XX leukemia or in manufacturing medicaments for the treatment of such
XX diseases. The present sequence represents the heavy chain of human anti-
XX CD40 monoclonal antibody CHIR-5.9.
XX
SQ Sequence 474 AA;
Query Match 89.1%; Score 623; DB 9; Length 474;
Best Local Similarity 91.5%; Pred. No. 1.8e-48;
Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
QY 1 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVROMPGKLEWMIYPGSDTRY 60
DB 20 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVROMPGKLEWMIYPGSDTRY 79
QY 61 SPSFQQTATISADKSIISTAYLQWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVWG 120
DB 80 SPSFQQTATISADKSIISTAYLQWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVWG 135
QY 121 QGTTVTSS 129
DB 136 QGTTVTSS 144
RESULT 10
AEA18548

```

ID AEA18548 standard; protein; 474 AA.  
 AC AEA18548;  
 XX  
 DT 28-JUL-2005 (first entry)  
 DE Heavy chain of anti-CD40 antibody CHIR-5.9.  
 XX  
 KW cytostatic; gene therapy; neoplasm; solid tumor; CD40; heavy chain;  
 XX antibody CHIR-5.9; antibody therapy; ss.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "leader peptide"  
 FT Region 20..144  
 FT /note= "variable region"  
 FT Region 145..474  
 FT /note= "constant region"  
 XX  
 PN WO2005044305-A2.  
 XX  
 PD 19-MAY-2005.  
 XX  
 PF 04-NOV-2004; 2004WO-US036955.  
 XX  
 PR 04-NOV-2003; 2003US-0517337P.  
 PR 26-NOV-2003; 2003US-0525579P.  
 PR 27-APR-2004; 2004US-0565634P.  
 PR 27-APR-2004; 2004US-0565710P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PI Long L, Luqman M, Yabannavar A, Zaror I;  
 XX  
 DR WPI; 2005-346956/35.  
 XX  
 XX Treating human subjects for solid tumors that express CD40 cell-surface  
 PT antigen comprises administering to the subject an amount of a human  
 PT antagonist anti-CD40 monoclonal antibody that specifically binds to the  
 PT CD40 antigen.  
 XX  
 PS Claim 1; SEQ ID NO 7; 123pp; English.  
 XX  
 CC The specification describes a method of treating a human subject for a  
 CC solid tumor comprising carcinoma cells expressing CD40 antigen. The  
 CC method comprises administering to the subject an amount of a human anti-  
 CC CD40 monoclonal antibody that is capable of specifically binding to the  
 CC CD40 antigen, the monoclonal antibody being free of significant agonist  
 CC activity when bound to CD40 antigen. The method of the invention is  
 CC useful for treating solid tumors expressing the CD40 cell-surface  
 CC antigen, such as sarcomas or carcinoma of the lungs, breasts, ovary,  
 CC skin, colon or urinary bladder, or in manufacturing medicaments for the  
 CC treatment of such diseases. The present sequence represents the heavy  
 CC chain of anti-CD40 monoclonal antibody CHIR-5.9. This antibody represents  
 CC an antibody which can be used in the method of the invention.  
 XX  
 SQ Sequence 474 AA;  
 Query Match 89.1%; Score 623; DB 9; Length 474;  
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;  
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;  
 QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTFTYWGVRQMPGKLEWGMGIYPGSDTRY 60  
 DB 20 EVQLVQSGAEVKKPGESLKISCKGSGYSTFTYWGVRQMPGKLEWGMGIYPGSDTRY 79  
 QY 61 SPSPFGQQTISADKSIISTAYLQWSSLSKASDTAMTCARHVDVGATIGGYYTHGMDVWG 120  
 DB 80 SPSPFGQQTISADKSIISTAYLQWSSLSKASDTAMTCARHVDVGATIGGYYTHGMDVWG 135  
 QY 121 QGTTVTSS 129

DB 136 QGTTVTSS 144  
 |||||  
 RESULT 11  
 AEA18549  
 ID AEA18549 standard; protein; 474 AA.  
 XX  
 AC AEA18549;  
 XX  
 DT 28-JUL-2005 (first entry)  
 DE Variant of the heavy chain of anti-CD40 antibody CHIR-5.9.  
 XX  
 KW cytoetic; gene therapy; neoplasm; solid tumor; CD40; heavy chain;  
 XX antibody CHIR-5.9; antibody therapy; ss.  
 OS Synthetic.  
 XX  
 PN WO2005044305-A2.  
 XX  
 PD 19-MAY-2005.  
 XX  
 PF 04-NOV-2004; 2004WO-US036955.  
 XX  
 PR 04-NOV-2003; 2003US-0517337P.  
 PR 26-NOV-2003; 2003US-0525579P.  
 PR 27-APR-2004; 2004US-0565634P.  
 PR 27-APR-2004; 2004US-0565710P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PI Long L, Luqman M, Yabannavar A, Zaror I;  
 XX  
 DR WPI; 2005-346956/35.  
 XX  
 XX Treating human subjects for solid tumors that express CD40 cell-surface.  
 PT antigen comprises administering to the subject an amount of a human  
 PT antagonist anti-CD40 monoclonal antibody that specifically binds to the  
 PT CD40 antigen.  
 XX  
 PS Claim 1; SEQ ID NO 8; 123pp; English.  
 XX  
 CC The specification describes a method of treating a human subject for a  
 CC solid tumor comprising carcinoma cells expressing CD40 antigen. The  
 CC method comprises administering to the subject an amount of a human anti-  
 CC CD40 monoclonal antibody that is capable of specifically binding to the  
 CC CD40 antigen, the monoclonal antibody being free of significant agonist  
 CC activity when bound to CD40 antigen. The method of the invention is  
 CC useful for treating solid tumors expressing the CD40 cell-surface  
 CC antigen, such as sarcomas or carcinoma of the lungs, breasts, ovary,  
 CC skin, colon or urinary bladder, or in manufacturing medicaments for the  
 CC treatment of such diseases. The present sequence represents a variant of  
 CC the heavy chain of anti-CD40 monoclonal antibody CHIR-5.9, comprising a  
 CC Ser for Ala substitution at site 158. This antibody represents an  
 CC antibody which can be used in the method of the invention.  
 XX  
 SQ Sequence 474 AA;  
 Query Match 89.1%; Score 623; DB 9; Length 474;  
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;  
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;  
 QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTFTYWGVRQMPGKLEWGMGIYPGSDTRY 60  
 DB 20 EVQLVQSGAEVKKPGESLKISCKGSGYSTFTYWGVRQMPGKLEWGMGIYPGSDTRY 79  
 QY 61 SPSPFGQQTISADKSIISTAYLQWSSLSKASDTAMTCARHVDVGATIGGYYTHGMDVWG 120  
 DB 80 SPSPFGQQTISADKSIISTAYLQWSSLSKASDTAMTCARHVDVGATIGGYYTHGMDVWG 135  
 QY 121 QGTTVTSS 129  
 |||||

Db 136 QGTTVTVSS 144

RESULT 12  
AEA10642  
ID AEA10642 standard; protein; 474 AA.  
XX AEA10642;  
AC AEA10642;  
XX 28-JUL-2005 (first entry)  
DT Human anti-CD40 monoclonal antibody 5.9 heavy chain variant protein.  
DE multiple myeloma; hematological disease; immune disorder;  
XX antibody therapy; cytostatic; gene therapy; CD40; monoclonal antibody;  
KW heavy chain.  
KW heavy chain.  
XX Homo sapiens.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Region 1..19  
FT /note= "Leader region"  
FT Region 20..144  
FT /note= "Variable region"  
FT Region 145..474  
FT /note= "Constant region"  
FT Misc-difference 158  
FT /note= "Wild-type Ala has been substituted by Ser"  
XX WO2005044855-A2.  
PN 19-MAY-2005.  
XX 04-NOV-2004; 2004WO-US037281.  
XX 04-NOV-2003; 2003US-0517337P.  
PR 26-NOV-2003; 2003US-0525579P.  
PR 26-APR-2004; 2004US-0565709P.  
PR 27-APR-2004; 2004US-0565710P.  
XX (CHIR ) CHIRON CORP.  
XX Long L, Luqman M, Yabannavar A, Zaror I;  
PI WPI; 2005-347055/35.  
XX Treating human subjects for multiple myeloma comprises administering to  
PT the subject an amount of a human antagonist anti-CD40 monoclonal antibody  
PT that specifically binds to the CD40 antigen.  
XX Claim 1; SEQ ID NO 8; 115pp; English.  
XX The invention relates to a novel method for treating a human subject for  
CC multiple myeloma comprising administering to the subject an amount of a  
CC human anti-CD40 monoclonal antibody that specifically binds to a human  
CC CD40 antigen expressed on the surface of a human CD40-expressing cell and  
CC that is free of significant agonist activity, where the binding of the  
CC antibody to the CD40 antigen expressed on the surface of the cell results  
CC in inhibition of the growth or differentiation of the cell. Multiple  
CC myeloma is a B-cell malignancy characterized by latent accumulation of  
CC secretory plasma cells in the bone marrow, these cells having a low  
CC proliferative index and an extended life span. The disease ultimately  
CC attacks bones and bone marrow, resulting in multiple tumors and regions  
CC throughout the skeletal system. The method of the invention demonstrates  
CC cytostatic and gene therapy applications and may be useful for treating  
CC multiple myeloma or in manufacturing medicaments for the treatment of  
CC such a disease. The current sequence is that of the human anti-CD40  
CC monoclonal antibody 5.9 heavy chain variant protein of the invention.  
XX Sequence 474 AA;  
SQ

Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;  
QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPKGLWMGIIYPGSDTRY 60  
DB AEA10642  
DB 20 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPKGLWMGIIYPGSDTRY 79  
QY 61 SPSPGQATISADKSIISTAYLQWSSLKASDTAMTYCARHVDVGATIGYGYHHGMVDVWG 120  
DB 80 SPSPGQATISADKSIISTAYLQWSSLKASDTAMTYCARHVDVGATIGYGYHHGMVDVWG 135  
QY 121 QGTTVTVSS 129  
DB 136 QGTTVTVSS 144

RESULT 13  
AEA10641  
ID AEA10641 standard; protein; 474 AA.  
XX AEA10641;  
AC AEA10641;  
XX 28-JUL-2005 (first entry)  
DT Human anti-CD40 monoclonal antibody 5.9 heavy chain protein.  
DE multiple myeloma; hematological disease; immune disorder;  
XX antibody therapy; cytostatic; gene therapy; CD40; monoclonal antibody;  
KW heavy chain.  
KW heavy chain.  
XX Homo sapiens.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Region 1..19  
FT /note= "Leader region"  
FT Region 20..144  
FT /note= "Variable region"  
FT Region 145..474  
FT /note= "Constant region"  
FT Misc-difference 158  
FT /note= "A variant exists in which wild-type Ala may be  
FT substituted by Ser"  
XX WO2005044855-A2.  
PN 19-MAY-2005.  
XX 04-NOV-2004; 2004WO-US037281.  
XX 04-NOV-2003; 2003US-0517337P.  
PR 26-NOV-2003; 2003US-0525579P.  
PR 26-APR-2004; 2004US-0565709P.  
PR 27-APR-2004; 2004US-0565710P.  
XX (CHIR ) CHIRON CORP.  
XX Long L, Luqman M, Yabannavar A, Zaror I;  
PI WPI; 2005-347055/35.  
XX Treating human subjects for multiple myeloma comprises administering to  
PT the subject an amount of a human antagonist anti-CD40 monoclonal antibody  
PT that specifically binds to the CD40 antigen.  
XX Claim 1; SEQ ID NO 7; 115pp; English.  
XX The invention relates to a novel method for treating a human subject for  
CC multiple myeloma comprising administering to the subject an amount of a  
CC human anti-CD40 monoclonal antibody that specifically binds to a human  
CC CD40 antigen expressed on the surface of a human CD40-expressing cell and  
CC that is free of significant agonist activity, where the binding of the  
CC antibody to the CD40 antigen expressed on the surface of the cell results  
CC in inhibition of the growth or differentiation of the cell. Multiple  
CC myeloma is a B-cell malignancy characterized by latent accumulation of  
CC secretory plasma cells in the bone marrow, these cells having a low  
CC proliferative index and an extended life span. The disease ultimately  
CC attacks bones and bone marrow, resulting in multiple tumors and regions  
CC throughout the skeletal system. The method of the invention demonstrates  
CC cytostatic and gene therapy applications and may be useful for treating  
CC multiple myeloma or in manufacturing medicaments for the treatment of  
CC such a disease. The current sequence is that of the human anti-CD40  
CC monoclonal antibody 5.9 heavy chain variant protein of the invention.  
XX Sequence 474 AA;  
SQ

Query Match 89.1%; Score 623; DB 9; Length 474;  
Best Local Similarity 91.5%; Pred. No. 1.8e-48;

CC secretory plasma cells in the bone marrow, these cells having a low  
 CC proliferative index and an extended life span. The disease ultimately  
 CC attacks bones and bone marrow, resulting in multiple tumors and regions  
 CC throughout the skeletal system. The method of the invention demonstrates  
 CC cytostatic and gene therapy applications and may be useful for treating  
 CC multiple myeloma or in manufacturing medicaments for the treatment of  
 CC such a disease. The current sequence is that of the human anti-CD40  
 CC monoclonal antibody 5.9 heavy chain protein of the invention.  
 XX  
 XX Sequence 474 AA;

Query Match 89.1%; Score 623; DB 9; Length 474;  
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;  
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;  
 QY 1 EVLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVRQMPKGLWGMIIYPGSDTRY 60  
 DB 20 EVLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVRQMPKGLWGMIIYPGSDTRY 79  
 QY 61 SPSPGQQTISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120  
 DB 80 SPSPGQQTISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 135  
 QY 121 QGTTVTSS 129  
 DB 136 QGTTVTSS 144

RESULT 14  
 AED25714  
 ID AED25714 standard; protein; 474 AA.

AC AED25714;

DT 01-DEC-2005 (first entry)

DE Monoclonal anti-CD40-antibody CHIR-5.9 heavy chain.

KW cytostatic; monoclonal antibody; antibody therapy; cancer; neoplasm;  
 KW CHIR-5.9; heavy chain.

OS Homo sapiens.

Key Location/Qualifiers

Peptide 1..19

Protein /label= Signal\_peptide

Protein 20..474

Protein /note= "Mature monoclonal anti-CD40-antibody CHIR-5.9  
 heavy chain"

Region 20..144

Region /note= "Monoclonal anti-CD40-antibody CHIR-5.9 heavy  
 chain variable region"

Region 145..474

Region /note= "Monoclonal anti-CD40-antibody CHIR-5.9 heavy  
 chain constant region"

XX WO200504294-A2.

XX 19-MAY-2005.

XX 04-NOV-2004; 2004WO-US036958.

XX 04-NOV-2003; 2003US-0517337P.

XX 26-NOV-2003; 2003US-0525579P.

XX 27-APR-2004; 2004US-0565710P.

XX (CHIR ) CHIRON CORP.

XX Long L, Luqman M, Yabannavar A, Zaror I, Hurst D;

XX Lopes De Menezes DE;

XX WPI; 2005-746884/76.

XX

PT Treating human subject for cancer comprising neoplastic cells expressing  
 PT CD40 antigen, by administering combination therapy including  
 PT administration of anti-CD40 antibody e.g. CHIR-5.9, in combination with  
 PT interleukin-2, to subject.

XX Claim 1; SEQ ID NO 7; 204pp; English.

XX The invention describes a method of treating (M1) a human subject for  
 CC cancer comprising neoplastic cells expressing CD40 antigen. The method  
 CC involves administering to the subject, a combination therapy including  
 CC administration of an anti-CD40 antibody in combination with an  
 CC interleukin-2 (IL-2), where the anti-CD40 antibody is the monoclonal  
 CC antibody CHIR-5.9 or CHIR-12.12. (M1) is useful for treating a human  
 CC subject for cancer comprising neoplastic cells expressing CD40 antigen,  
 CC where the cancer is a B cell-related cancer or solid tumor. The B cell-  
 CC related cancer is chosen from non-Hodgkin's lymphoma, chronic lymphocytic  
 CC leukemia, multiple myeloma, B cell lymphoma, high-grade B cell lymphoma,  
 CC intermediate-grade B cell lymphoma, low-grade B cell lymphoma, B cell  
 CC acute lymphoblastic leukemia, myeloblastic leukemia, Hodgkin's disease,  
 CC plasmacytoma, follicular lymphoma, follicular small cleaved lymphoma,  
 CC follicular large cell lymphoma, follicular mixed small cleaved lymphoma,  
 CC diffuse small cleaved cell lymphoma, diffuse small lymphocytic lymphoma,  
 CC prolymphocytic leukemia, lymphoplasmacytic lymphoma, marginal zone  
 CC lymphoma, mucosal associated lymphoid tissue lymphoma, monocytoid B cell  
 CC lymphoma, splenic lymphoma, hairy cell leukemia, diffuse large cell  
 CC lymphoma, mediastinal large B cell lymphoma, lymphomatoid granulomatosis,  
 CC intravascular lymphomatosis, diffuse mixed cell lymphoma, AIDS-related  
 CC cell lymphoma, immunoblastic lymphoma, Burkitt's lymphoma, AIDS-related  
 CC lymphoma and mantle cell lymphoma. The solid tumor is chosen from urinary  
 CC bladder carcinoma, breast carcinoma, liver carcinoma, gastric carcinoma,  
 CC colon carcinoma, prostate cancer, renal cell carcinoma, nasopharyngeal  
 CC carcinoma, squamous cell carcinoma, thyroid papillary carcinoma,  
 CC melanoma, ovarian carcinoma, lung carcinoma, cervical carcinoma and  
 CC sarcomas. This is the amino acid sequence of human monoclonal anti-CD40-  
 CC antibody CHIR-5.9 heavy chain.

XX Sequence 474 AA;

Query Match 89.1%; Score 623; DB 9; Length 474;

Best Local Similarity 91.5%; Pred. No. 1.8e-48;

Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 1 EVLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVRQMPKGLWGMIIYPGSDTRY 60  
 DB 20 EVLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVRQMPKGLWGMIIYPGSDTRY 79  
 QY 61 SPSPGQQTISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120  
 DB 80 SPSPGQQTISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 135  
 QY 121 QGTTVTSS 129  
 DB 136 QGTTVTSS 144

RESULT 15

AED25715

ID AED25715 standard; protein; 474 AA.

XX AED25715;

XX 01-DEC-2005 (first entry)

XX Monoclonal anti-CD40-antibody CHIR-5.9 heavy chain A1585.

XX cytostatic; monoclonal antibody; antibody therapy; cancer; neoplasm;  
 KW CHIR-5.9; heavy chain; mutein.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 158

XX /note= "Wild type Ala substituted by Ser"

Search completed: April 25, 2007, 04:05:19  
Job time : 111.873 secs

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XX WO2005044294-A2.
XX
XX 19-MAY-2005.
XX
XX 04-NOV-2004; 2004WO-US036958.
XX
XX 04-NOV-2003; 2003US-0517337P.
XX
XX 26-NOV-2003; 2003US-0525579P.
XX
XX 27-APR-2004; 2004US-0565710P.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Long I, Lugman M, Yabannavar A, Zaror I, Hurst D;
XX Lopes De Menezes DE;
XX
XX WPI; 2005-746884/76.
XX
XX Treating human subject for cancer comprising neoplastic cells expressing
XX CD40 antigen, by administering combination therapy including
XX administration of anti-CD40 antibody e.g. CHIR-5.9, in combination with
XX interleukin-2, to subject.
XX
XX Claim 1; SEQ ID NO 8; 204pp; English.
XX
XX The invention describes a method of treating (M1) a human subject for
XX cancer comprising neoplastic cells expressing CD40 antigen. The method
XX involves administering to the subject, a combination therapy including
XX administration of an anti-CD40 antibody in combination with an
XX interleukin-2 (IL-2), where the anti-CD40 antibody is the monoclonal
XX antibody CHIR-5.9 or CHIR-12.12. (M1) is useful for treating a human
XX subject for cancer comprising neoplastic cells expressing CD40 antigen,
XX where the cancer is a B cell-related cancer or solid tumor. The B cell-
XX related cancer is chosen from non-Hodgkin's lymphoma, chronic lymphocytic
XX leukemia, multiple myeloma, B cell lymphoma, high-grade B cell lymphoma,
XX intermediate-grade B cell lymphoma, low-grade B cell lymphoma, B cell
XX acute lymphoblastic leukemia, myeloblastic leukemia, Hodgkin's disease,
XX plasmacytoma, follicular lymphoma, follicular small cleaved lymphoma,
XX follicular large cell lymphoma, follicular mixed small cleaved lymphoma,
XX diffuse small cleaved cell lymphoma, diffuse small lymphocytic lymphoma,
XX prolymphocytic leukemia, lymphoplasmacytic lymphoma, marginal zone
XX lymphoma, mucosal associated lymphoid tissue lymphoma, monocytoid B cell
XX lymphoma, splenic lymphoma, hairy cell leukemia, diffuse large cell
XX lymphoma, mediastinal large B cell lymphoma, lymphomatoid granulomatosis,
XX intravascular lymphomatosis, diffuse mixed cell lymphoma, diffuse large
XX cell lymphoma, immunoblastic lymphoma, Burkitt's lymphoma, AIDS-related
XX lymphoma and mantle cell lymphoma. The solid tumor is chosen from urinary
XX bladder carcinoma, breast carcinoma, liver carcinoma, gastric carcinoma,
XX colon carcinoma, prostate cancer, renal cell carcinoma, nasopharyngeal
XX carcinoma, squamous cell carcinoma, thyroid papillary carcinoma,
XX melanoma, ovarian carcinoma, lung carcinoma, cervical carcinoma and
XX sarcomas. This is the amino acid sequence of human monoclonal anti-CD40-
XX antibody CHIR-5.9 heavy chain A158S.
XX
XX Sequence 474 AA;
XX
XX Query Match      89.1%; Score 623; DB 9; Length 474;
XX Best Local Similarity 91.5%; Pred. No. 1.8e-48;
XX Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
XX
XX QY      1 EVQLVDSGAEVKKPGESLKISCKSGYSFTSYWIGWVRQMPGKLEWGMGIYPGDSDTRY 60
XX      |||||
XX Db      20 EVQLVDSGAEVKKPGESLKISCKSGYSFTSYWIGWVRQMPGKLEWGMGIYPGDSDTRY 79
XX
XX QY      61 SPSPFQQTATISADKSIISTAYLWSSLKASDTAMYYCARHVDVGATIGGVYVYHGMVDVWG 120
XX      |||||
XX Db      80 SPSPFQQTATISADKSIISTAYLWSSLKASDTAMYYCAR----GTAAGRDYVYVYHGMVDVWG 135
XX
XX QY      121 QGTTVTVSS 129
XX      |||||
XX Db      136 QGTTVTVSS 144
```

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 10 Seconds  
(without alignments)  
1261.509 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EVQLVQSGAEVKKPGESLK1.....YYHHGMDVWGQGTITVSS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609.5	87.2	136	2 A49047	Ig heavy chain V r
2	587.5	84.0	134	2 PH1422	Ig heavy chain V r
3	576.5	82.5	139	2 PH1558	Ig heavy chain V r
4	574	82.1	123	2 C36006	Ig heavy chain V r
5	564	80.7	113	2 PH1428	Ig heavy chain V r
6	561	80.3	123	2 S38492	Ig heavy chain - h
7	561	80.3	144	2 PH1563	Ig heavy chain V r
8	558	79.8	127	2 PH1414	Ig heavy chain V r
9	553.5	79.2	141	2 S31685	Ig heavy chain V r
10	552.5	79.0	147	2 PH1561	Ig heavy chain V r
11	547	78.3	123	2 PH1423	Ig heavy chain V r
12	546	78.1	127	2 PH1415	Ig heavy chain V r
13	546	78.1	136	2 PH1559	Ig heavy chain V r
14	545	78.0	127	2 PH1420	Ig heavy chain V r
15	542.5	77.6	126	2 PH1419	Ig heavy chain V r
16	539	77.1	138	2 PH1565	Ig heavy chain V r
17	536.5	76.8	126	2 PH1417	Ig heavy chain V r
18	536.5	76.8	126	2 PH1418	Ig heavy chain V r
19	529.5	75.8	126	2 PH1416	Ig heavy chain V r
20	529	75.7	117	2 S19670	Ig heavy chain V r
21	528	75.5	123	2 PH1413	Ig heavy chain V r
22	527.5	75.5	126	2 PH1424	Ig heavy chain V r
23	527	75.4	128	2 S16685	Ig heavy chain V r
24	523	74.8	138	2 PH1564	Ig heavy chain V r
25	521	74.5	127	2 PH1411	Ig heavy chain V r
26	519	74.2	98	2 S26907	Ig heavy chain V r
27	519	74.2	101	2 S12424	Ig heavy chain V r
28	519	74.2	102	2 PH1279	Ig heavy chain V r
29	519	74.2	115	2 PH1557	Ig heavy chain V r

30	517	74.0	119	2 S36257	Ig heavy chain V r
31	516	73.8	102	2 PH1266	Ig heavy chain V r
32	516	73.8	102	2 PH1252	Ig heavy chain V r
33	515	73.7	117	2 S19669	Ig heavy chain V r
34	514	73.5	101	2 S12428	Ig heavy chain V r
35	514	73.5	117	2 A28846	Ig heavy chain pre
36	513	73.4	102	2 PH1281	Ig heavy chain V r
37	513	73.4	102	2 PH1271	Ig heavy chain V r
38	513	73.4	102	2 PH1278	Ig heavy chain V r
39	512	73.2	109	2 PH1672	Ig heavy chain V r
40	511	73.1	102	2 PH1254	Ig heavy chain V r
41	510.5	73.0	122	2 FC4800	anti-SS-A/Ro 60K p
42	510	73.0	102	2 PH1258	Ig heavy chain V r
43	510	73.0	144	2 E41287	Ig heavy chain pre
44	508.5	72.7	137	2 PH1562	Ig heavy chain V r
45	507.5	72.6	122	2 PH1426	Ig heavy chain V r

#### ALIGNMENTS

##### RESULT 1

A49047

Ig heavy chain V region (monoclonal striational autoantibody StrAB SA-1A VH) - human (fr  
C;Species: Homo sapiens (man)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Mar-1998  
C;Accession: A49047  
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.  
Eur. J. Immunol. 22, 2231-2236, 1992  
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes  
A;Reference number: A49047; MUID:92387224; PMID:1516616  
A;Accession: A49047  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-136 <VIC>  
A;Cross-references: UNIPARC:UPI0000176C6A  
A;Experimental source: thymic B lymphocytes  
A;Note: sequence extracted from NCBI backbone (NCBIN:113206, NCBIPI:113207)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match	87.2%	Score	609.5;	DB 2;	Length	136;			
Best Local Similarity	87.4%;	Pred. No.	6.9e-48;						
Matches	118;	Conservative	4;	Mismatches	4;	Indels	9;	Gaps	3;
Qy	1	EVQLVQSGAEVKKPGESLKISKSGSYFTSYWVQMPGKGLWNGIYPGDS	60						
Db	5	EVQLVQSGAEVKKPGESLKISKSGSYFTSYWVQMPGKGLWNGIYPGDS	64						
Qy	61	SPSFQQAATISADKSIATYQWSSLKASDTAMYCAR----	HVDVQATIGGYY--	114					
Db	65	SPSFQQAATISADKSIATYQWSSLKASDTAMYCARQSYGYDFRS--	GYYPAYYYY	121					
Qy	115	GMDVWGQGTITVVS	129						
Db	122	GMDVWGQGTITVVS	136						

##### RESULT 2

PH1422

Ig heavy chain V region (clone P3-69) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C;Accession: PH1422  
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.  
J. Exp. Med. 177, 99-107, 1993  
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s  
dermatitis.  
A;Reference number: PH1409; MUID:93115676; PMID:8418213  
A;Accession: PH1422  
A;Molecule type: mRNA  
A;Residues: 1-134 <VAN>  
A;Cross-references: UNIPARC:UPI0000176A2E



A:Experimental source: PBMC  
A:Note: the authors translated the codon ATG for residue 93 as Thr  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 587.5; DB 2; Length 134;  
Best Local Similarity 85.6%; Pred. No. 6.4e-46;  
Matches 113; Conservative 3; Mismatches 11; Indels 5; Gaps 2;

QY 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWGWVROMPGKLEWNGIIPGSDTRY 60  
DB 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWGWVROMPGKLEWNGIIPGSDTRY 60  
QY 61 SPFGQQTATISADKSIKSTAYLQWSSLKASDTAMYCARH---VDVGATIGGYYYHGM 117  
DB 61 SPFGQQTATISADKSIKSTAYLQWSSLKASDTAMYCARHGMVEYYYGSGSDYIIY--MD 118  
QY 118 VNGQGTITVSS 129  
DB 119 VNGKGTITVSS 130

RESULT 3  
PH1558  
Ig heavy chain V region (clone DOB) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 16-Aug-1996  
C:Accession: PH1558  
R:Rassenti, L.Z.; Kipps, T.J.  
J. Exp. Med. 177, 1039-1046, 1993  
A:Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymphocytic leukemia  
A:Reference number: PH1557; MUID:93210459; PMID:7681468  
A:Accession: PH1558  
A:Molecule type: DNA  
A:Residues: 1-139 <RAS>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:32-115/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 576.5; DB 2; Length 139;  
Best Local Similarity 85.3%; Pred. No. 6.5e-45;  
Matches 110; Conservative 1; Mismatches 11; Indels 7; Gaps 1;

QY 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWGWVROMPGKLEWNGIIPGSDTRY 60  
DB 18 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWGWVROMPGKLEWNGIIPGSDTRY 77  
QY 61 SPFGQQTATISADKSIKSTAYLQWSSLKASDTAMYCARHVDVGATIGGYYYHGM 120  
DB 78 SPFGQQTATISADKSIKSTAYLQWSSLKASDTAMYCARSSSG-----YYSNFDYWG 130  
QY 121 QGTITVSS 129  
DB 131 QGTLTVSS 139

RESULT 4  
C36006  
Ig heavy chain V region (83p2) - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998  
C:Accession: C36006  
R:Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A:Reference number: A36005; MUID:90349571; PMID:21117273  
A:Accession: C36006  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-123 <SCH>  
A:Cross-references: UNIPARC:UPI0000176C49; GB:M34022

C:Genetics:  
A:Gene: GDB:IGH0; IGHY1  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 574; DB 2; Length 123;  
Best Local Similarity 85.3%; Pred. No. 9.6e-45;  
Matches 110; Conservative 5; Mismatches 8; Indels 6; Gaps 2;

QY 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWGWVROMPGKLEWNGIIPGSDTRY 60  
DB 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWGWVROMPGKLEWNGIIPGSDTRY 60  
QY 61 SPFGQQTATISADKSIKSTAYLQWSSLKASDTAMYCARHVDVGATIGGYYYHGM 120  
DB 61 SPFGQQTATISADKSIKSTAYLQWSSLKASDTAMYCARH---NSQTGSLWYF---DLWG 114  
QY 121 QGTITVSS 129  
DB 115 QGTLTVSS 123

RESULT 5  
PH1428  
Ig heavy chain V region (clone VH5-1R1) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 28-May-1999  
C:Accession: PH1428  
R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.  
J. Exp. Med. 177, 99-107, 1993  
A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of structural mutations  
A:Reference number: PH1409; MUID:93115676; PMID:8418213  
A:Accession: PH1428  
A:Molecule type: mRNA  
A:Residues: 1-113 <VAN>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 564; DB 2; Length 113;  
Best Local Similarity 84.5%; Pred. No. 7e-44;  
Matches 109; Conservative 0; Mismatches 4; Indels 16; Gaps 1;

QY 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWGWVROMPGKLEWNGIIPGSDTRY 60  
DB 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWGWVROMPGKLEWNGIIPGSDTRY 60  
QY 61 SPFGQQTATISADKSIKSTAYLQWSSLKASDTAMYCARHVDVGATIGGYYYHGM 120  
DB 61 SPFGQQTATISADKSIKSTAYLQWSSLKASDTAMYCAR-----AFDVGW 104  
QY 121 QGTITVSS 129  
DB 105 QGTMVTSS 113

RESULT 6  
S38492  
Ig heavy chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S38492  
R:Wark, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Thorpe, S.  
Submitted to the EMBL Data Library, June 1993  
A:Description: Human antibody fragments specific for human blood group antigens from a phage display library  
A:Reference number: S38488  
A:Accession: S38492  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-123 <VAR>

A;Cross-references: UNIPARC:UPI000011654D; EMBL:Z23034; NID:9414031; PIDN:CAA80569.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 561; DB 2; Length 123;  
Best Local Similarity 83.2%; Pred. No. 1.4e-43;  
Matches 109; Conservative 3; Mismatches 9; Indels 10; Gaps 2;

QY 1 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWIGVRQMPGKLEWNGIIPGDSPTRY 60

Db 1 QVQLVSGAEVKKPGESLKISCKSGYSFTSYWIGVRQMPGKLEWNGIIPGDSPTRY 60

QY 61 SPSPFOQATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVWG 118

Db 61 SPSPFOQATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVWG 112

QY 119 WQGTITVTSS 129

Db 113 WGRGLTIVTSS 123

#### RESULT 7

PH1563

Ig heavy chain V region (clone PET) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 21-Jan-2000  
C;Accession: PH1563  
R;Rassenti, L.Z.; Kippes, T.J.  
J. Exp. Med. 177, 1039-1046, 1993  
A;Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymphoma  
A;Reference number: PH1557; MUID:93210459; PMID:7681468  
A;Accession: PH1563

A:Molecule type: DNA  
A:Residues: 1-144 <VAR>

A;Cross-references: UNIPARC:UPI0000176963  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;32-115/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 561; DB 2; Length 144;  
Best Local Similarity 84.5%; Pred. No. 1.7e-43;  
Matches 109; Conservative 3; Mismatches 15; Indels 2; Gaps 1;

QY 1 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWIGVRQMPGKLEWNGIIPGDSPTRY 60

Db 18 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWISWRQMPGKLEWNGRIDPSDYTNV 77

QY 61 SPSPFOQATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120

Db 78 SPSPFOGHVITISADKSIISTAYLQWSSLSKASDTAMYCARLLYGAAAWGYYHYHGMVWG 135

QY 121 QGTITVTSS 129

Db 136 KGTITVTSS 144

#### RESULT 8

PH1414

Ig heavy chain V region (clone PI-54) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999  
C;Accession: PH1414  
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.  
J. Exp. Med. 177, 99-107, 1993  
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of somatic mutations.  
A;Reference number: PH1409; MUID:93115676; PMID:8418213  
A;Accession: PH1414  
A:Molecule type: mRNA  
A:Residues: 1-127 <VAR>

A;Cross-references: UNIPARC:UPI000017694E

A;Experimental source: PBMC

A;Note: the authors translated the codon TTG for residue 119 as Met

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 558; DB 2; Length 127;  
Best Local Similarity 84.5%; Pred. No. 2.7e-43;  
Matches 109; Conservative 3; Mismatches 11; Indels 6; Gaps 2;

QY 1 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWIGVRQMPGKLEWNGIIPGDSPTRY 60

Db 1 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWIGVRQMPGKLEWNGIIPGDSPTRY 60

QY 61 SPSPFOQATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120

Db 61 SPSPFOQATISADKSIISTAYLQWSSLSKATDTAMYCARHVDVGATIGGYYHYHGMVWG 114

QY 121 QGTITVTSS 129

Db 115 QGTITVTSS 123

#### RESULT 9

S31685

Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C;Accession: S31685  
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31685  
A;Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-141 <CUI>  
A;Cross-references: UNIPARC:UPI0000116462; EMBL:Z14183; NID:931033; PIDN:CAA78552.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 553.5; DB 2; Length 141;  
Best Local Similarity 82.9%; Pred. No. 7.7e-43;  
Matches 107; Conservative 3; Mismatches 12; Indels 7; Gaps 2;

QY 1 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWIGVRQMPGKLEWNGIIPGDSPTRY 60

Db 20 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWISWRQMPGKLEWNGRIDPSDYTNV 79

QY 61 SPSPFOQATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120

Db 80 SPSPFOGHVITISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVWG 132

QY 121 QGTITVTSS 129

Db 133 KGTITVTSS 141

#### RESULT 10

PH1561

Ig heavy chain V region (clone CAV) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 21-Jan-2000  
C;Accession: PH1561  
R;Rassenti, L.Z.; Kippes, T.J.  
J. Exp. Med. 177, 1039-1046, 1993  
A;Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymphoma  
A;Reference number: PH1557; MUID:93210459; PMID:7681468  
A;Accession: PH1561  
A:Molecule type: DNA  
A:Residues: 1-147 <RAS>

A;Cross-references: UNIPARC:UPI0000176961  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;32-115/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 552.5; DB 2; Length 147;  
Best Local Similarity 83.2%; Pred. No. 9.9e-43;  
Matches 109; Conservative 4; Mismatches 15; Indels 3; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISKCKSGYSFTSYWIGVVRQMPGKLEWMGIIYPGDSSTRY 60  
DB 18 EVQLVQSGAEVKKPGESLKISKCKSGYSFTSYWIGVVRQMPGKLEWMGRIDPSYNYI 77  
QY 61 SPSPGQATISADKSIKTAYLQWSSLKASDTAMYCARHVDVCGATIG--GYTYYHGMVDV 118  
DB 78 SPSPGQVTTISADKSIKTAYLQWSSLKASDTAMYCARQIAGIAAGWGPYYIYV 136  
QY 119 WQGTITVTVSS 129  
DB 137 WKGITVTVSS 147

RESULT 11  
PHI423  
Ig heavy chain V region (clone P3-9) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999  
C;Accession: PHI423  
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.  
J. Exp. Med. 177, 99-107, 1993  
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.  
A;Reference number: PHI409; MUID:93115676; PMID:8418213  
A;Accession: PHI423  
A;Molecule type: mRNA  
A;Residues: 1-123 <VAN>  
A;Cross-references: UNIPARC:UPI0000176961  
A;Experimental source: BMC  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 547; DB 2; Length 123;  
Best Local Similarity 80.6%; Pred. No. 2.6e-42;  
Matches 104; Conservative 4; Mismatches 11; Indels 10; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISKCKSGYSFTSYWIGVVRQMPGKLEWMGIIYPGDSSTRY 60  
DB 1 EVQLVQSGAEVKKPGESLKISKCKSGYSFTSYWIAVVRQMPGKLEWMGIIYPGDSSTRY 60  
QY 61 SPSPGQATISADKSIKTAYLQWSSLKASDTAMYCARHVDVCGATIGGYTYYHGMVDV 120  
DB 61 SPSPGQVTTISADKSIKTAYLQWSSLKASDTAIYCARHAD-----NFDWFQIW 110  
QY 121 QGTITVTVSS 129  
DB 111 QGTIVTVSS 119

RESULT 12  
PHI415  
Ig heavy chain V region (clone P1-57) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C;Accession: PHI415  
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.  
J. Exp. Med. 177, 99-107, 1993  
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.  
A;Reference number: PHI409; MUID:93115676; PMID:8418213  
A;Accession: PHI415  
A;Molecule type: mRNA  
A;Residues: 1-127 <VAN>

A;Cross-references: UNIPARC:UPI000017694F  
A;Experimental source: BMC  
A;Note: the authors translated the codon TTG for residue 118 as Met  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 546; DB 2; Length 127;  
Best Local Similarity 83.7%; Pred. No. 3.3e-42;  
Matches 108; Conservative 2; Mismatches 13; Indels 6; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISKCKSGYSFTSYWIGVVRQMPGKLEWMGIIYPGDSSTRY 60  
DB 1 EVQLVQSGAEVKKPGESLKISKCKSGYSFTSYWIGVVRQMPGKLEWMVVIYPGDSSTRY 60  
QY 61 SPSPGQATISADKSIKTAYLQWSSLKASDTAMYCARHVDVCGATIGGYTYYHGMVDV 120  
DB 61 SPSPGQVTTISADKSIKTAYLQWSSLKASDTAMYCARR-DYGD-----YQSTGTFDPWG 114  
QY 121 QGTITVTVSS 129  
DB 115 QGTIVTVSS 123

RESULT 13  
PHI559  
Ig heavy chain V region (clone HAM) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 21-Jan-2000  
C;Accession: PHI559  
R;Rassenti, L.Z.; Kipps, T.J.  
J. Exp. Med. 177, 1039-1046, 1993  
A;Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymphocytic leukemia.  
A;Reference number: PHI557; MUID:93210459; PMID:7681468  
A;Accession: PHI559  
A;Molecule type: DNA  
A;Residues: 1-136 <RAS>  
A;Cross-references: UNIPARC:UPI0000176A21  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;32-115/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 546; DB 2; Length 136;  
Best Local Similarity 82.2%; Pred. No. 3.5e-42;  
Matches 106; Conservative 2; Mismatches 11; Indels 10; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISKCKSGYSFTSYWIGVVRQMPGKLEWMGIIYPGDSSTRY 60  
DB 18 EVQLVQSGAEVKKPGESLKISKCKSGYSFTSYWIGVVRQMPGKLEWMGIIYPGDSSTRY 77  
QY 61 SPSPGQATISADKSIKTAYLQWSSLKASDTAMYCARHVDVCGATIGGYTYYHGMVDV 120  
DB 78 SPSPGQVTTISADKSIKTAYLQWSSLKASDTAMYCAR-----LYGDFSTVDVWG 127  
QY 121 QGTITVTVSS 129  
DB 128 QGTIVTVSS 136

RESULT 14  
PHI420  
Ig heavy chain V region (clone P2-55) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999  
C;Accession: PHI420  
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.  
J. Exp. Med. 177, 99-107, 1993  
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.  
A;Reference number: PHI409; MUID:93115676; PMID:8418213  
A;Accession: PHI420  
A;Molecule type: mRNA  
A;Residues: 1-127 <VAN>

A;Cross-references: UNIPARC:UPI0000176B9A

A;Experimental source: PBMC

A;Note: the authors translated the codon CTT for residue 101 as Phe

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 545; DB 2; Length 127;  
 Best Local Similarity 79.8%; Pred. No. 4e-42;  
 Matches 103; Conservative 8; Mismatches 12; Indels 6; Gaps 1;  
 QY 1 EVOLVQSGAEVKKPGESLKISCKSGSYSTSYWIGWVROMPGKLEWNGIIPGDSDTRY 60  
 DB 1 EVOLVQSGAEVKKPGESLKISCKSGSYSTSYWIGWVROMPGKLEWNGIIPGDSDTRY 60  
 QY 61 SPSFQCGQATISADKSIATYLOWSSLSKASDTAMYCARHVDVCGATIGGYYHYHGMVDVWG 120  
 DB 61 SPSFQCGQATISADKSIATYLOWSSLSKASDTAMYCARHVDVCGATIGGYYHYHGMVDVWG 120  
 QY 121 QGTTVTVSS 129  
 DB 115 RGTLTVPVS 123

RESULT 15

PHI419

IG heavy chain V region (clone P2-54) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999

C;Accession: PHI419

R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.

J. Exp. Med. 177, 99-107, 1993

A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.

A;Reference number: PHI409; MUID:93115676; PMID:8418213

A;Accession: PHI419

A;Molecule type: mRNA

A;Residues: 1-126 <VAN>

A;Cross-references: UNIPARC:UPI0000176953

A;Experimental source: PBMC

A;Note: the authors translated the codon ACT for residue 107 as Ser

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 542.5; DB 2; Length 126;  
 Best Local Similarity 79.1%; Pred. No. 6.7e-42;  
 Matches 102; Conservative 9; Mismatches 11; Indels 7; Gaps 1;  
 QY 1 EVOLVQSGAEVKKPGESLKISCKSGSYSTSYWIGWVROMPGKLEWNGIIPGDSDTRY 60  
 DB 1 EVOLVQSGAEVKKPGESLKISCKSGSYSTSYWIGWVROMPGKLEWNGIIPGDSDTRY 60  
 QY 61 SPSFQCGQATISADKSIATYLOWSSLSKASDTAMYCARHVDVCGATIGGYYHYHGMVDVWG 120  
 DB 61 SPSFQCGQATISADKSIATYLOWSSLSKASDTAMYCARHVDVCGATIGGYYHYHGMVDVWG 120  
 QY 121 QGTTVTVSS 129  
 DB 114 QGTMVTVSS 122

Search completed: April 25, 2007, 04:06:39  
 Job time : 9.83898 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 88 Seconds  
(without alignments)  
1574.822 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EVQLVQSGAEVKKPGESLK.....YYHHGMVWGQGTITVSS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_8.4.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	441.5	63.2	475	Q5RE17_PONPY	Q5RE17 pongo pygma
2	435.5	62.3	159	Q9GSO0_HUMAN	Q9GSO0 homo sapien
3	418.5	59.9	118	Q921C4_MOUSE	Q921C4 mus musculus
4	407	58.2	479	Q3KQK2_MOUSE	Q3KQK2 mus musculus
5	403	57.7	244	Q65ZC8_HUMAN	Q65ZC8 homo sapien
6	398	56.9	483	Q521S1_MOUSE	Q521S1 mus musculus
7	395	56.5	614	Q7TMT6_MOUSE	Q7TMT6 mus musculus
8	394	56.4	458	Q5BJZ2_RAT	Q5BJZ2 rattus norv
9	392.5	56.2	617	Q4KML5_MOUSE	Q4KML5 mus musculus
10	391.5	56.0	124	Q9UL92_HUMAN	Q9UL92 homo sapien
11	391.5	56.0	613	Q8VCX7_MOUSE	Q8VCX7 mus musculus
12	390.5	55.9	500	Q9BRV0_HUMAN	Q9BRV0 homo sapien
13	389.5	55.7	143	Q24P9_MOUSE	Q24P9 mus musculus
14	388	55.5	468	Q5G9W9_MOUSE	Q5G9W9 mus musculus
15	387	55.4	121	HV01_MOUSE	P01745 mus musculus
16	386.5	55.3	143	Q91V67_MOUSE	Q91V67 mus musculus
17	385.5	55.2	498	Q6N041_HUMAN	Q6N041 homo sapien
18	384.5	55.0	145	Q924O6_MOUSE	Q924O6 mus musculus
19	384	54.9	119	Q9TL94_HUMAN	Q9TL94 homo sapien
20	383	54.8	168	Q8VDC9_MOUSE	Q8VDC9 mus musculus
21	382.5	54.7	143	Q924Q5_MOUSE	Q924Q5 mus musculus
22	382.5	54.7	482	Q2T9K9_MOUSE	Q2T9K9 mus musculus
23	382.5	54.7	590	Q4V9V8_MOUSE	Q4V9V8 mus musculus
24	382	54.6	125	Q9UL95_HUMAN	Q9UL95 homo sapien
25	382	54.6	146	Q924Q3_MOUSE	Q924Q3 mus musculus
26	382	54.6	474	Q8R3H6_MOUSE	Q8R3H6 mus musculus
27	382	54.6	481	Q91WT1_MOUSE	Q91WT1 mus musculus
28	381.5	54.5	145	Q924R4_MOUSE	Q924R4 mus musculus
29	381	54.5	142	Q924Q2_MOUSE	Q924Q2 mus musculus
30	381	54.5	144	Q924P5_MOUSE	Q924P5 mus musculus
31	381	54.5	470	Q7TMK1_MOUSE	Q7TMK1 mus musculus

Query Match

Best Local Similarity 63.2%; Score 441.5; DB 2; Length 475;

Matches 86; Conservative 16; Mismatches 23; Indels 3; Gaps 2;

32	380.5	54.4	145	2	Q924R3_MOUSE	Q924R3 mus musculus
33	380.5	54.4	484	2	Q3SYJ4_MOUSE	Q3SYJ4 mus musculus
34	379	54.2	146	2	Q924R8_MOUSE	Q924R8 mus musculus
35	378.5	54.1	143	2	Q924Q0_MOUSE	Q924Q0 mus musculus
36	378.5	54.1	145	2	Q924O9_MOUSE	Q924O9 mus musculus
37	378.5	54.1	482	2	Q8K172_MOUSE	Q8K172 mus musculus
38	378	54.1	119	2	Q9GYZ2_MOUSE	Q9GYZ2 mus musculus
39	378	54.1	120	1	HV03_MOUSE	P01747 mus musculus
40	377.5	54.0	145	2	Q924R1_MOUSE	Q924R1 mus musculus
41	377	53.9	147	2	Q925S3_MOUSE	Q925S3 mus musculus
42	377	53.9	480	2	Q6PJF1_HUMAN	Q6PJF1 homo sapien
43	377	53.9	598	2	Q568Y0_RAT	Q568Y0 rattus norv
44	376.5	53.9	139	1	HV07_MOUSE	P01751 mus musculus
45	376.5	53.9	143	2	Q924R7_MOUSE	Q924R7 mus musculus

#### ALIGNMENTS

RESULT 1

Q5RE17\_PONPY  
ID Q5RE17\_PONPY PRELIMINARY; PRT; 475 AA.  
AC Q5RE17;  
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.  
DT 21-DEC-2004, sequence version 1.  
DT 27-JUN-2006, entry version 19.  
DE Hypothetical protein DKFp469C2335.  
GN Name=DKFp469C2335;  
OS Pongo pygmaeus (Orangutan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
OC Catarrhini; Hominoidea; Pongo.  
OX NCBI\_TaxID=9600;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Kidney;  
RG The German cDNA Consortium;  
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
CC histocompatibility complex class I molecules (By similarity).  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL: CR857722; CAH89990.1; -; mRNA.  
CC SMR: Q5RE17; 21-475.  
CC GO: GO:0016021; C:integral to membrane; IEA.  
CC GO: GO:0016020; C:membrane; IEA.  
CC GO: GO:0030106; F:MHC class I receptor activity; IEA.  
CC GO: GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
CC GO: GO:0019883; P:antigen processing, endogenous antigen via . . . ; IEA.  
CC InterPro: IPR007110; IG-like.  
CC InterPro: IPR003597; IG\_C1-set.  
CC InterPro: IPR003006; IG\_MHC.  
CC InterPro: IPR003599; IG\_sub.  
CC InterPro: IPR013106; IG\_V-set.  
CC Pfam: PF07654; C1-set; 3.  
CC Pfam: PF07686; V-set; 1.  
CC SMART: SM00409; IG; 1.  
CC SMART: SM00407; IG1; 2.  
CC SMART: SM00406; IGV; 1.  
CC PROSITE: PS00835; IG\_LIKE; 4.  
CC PROSITE: PS00290; IG\_MHC; UNKNOWN 2.  
KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;  
KW Transmembrane.  
SQ SEQUENCE 475 AA; 51898 MW; 04BBDE096A2CD529 CRC64;

```

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVWQMPGKGLWGMGIYPGSDTRY 60
DB 20 DIQLVQSGAEVKKPGESLRISCKGSGYFTSYWIGVWQMPGKGLWGMIDPNSGTRY 79
QY 61 SPSPQOQATISADKSI STAYLOWSLKASDTAMYYCARHVDVVGATIGGYYHYHGMVWG 120
DB 80 NRSFEGHITISADMSISTAYLOWSLKASDAIYYCAR-LRLSGT--NSYHKRSYFPQWG 136
QY 121 QGTTTVSS 128
DB 137 QGTLIVS 144

RESULT 2
Q96QSO HUMAN
ID Q96QSO HUMAN PRELIMINARY; PRT; 159 AA.
AC Q96QSO;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 18-APR-2006, entry version 21.
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tilson M.D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY039025; AAK82649.1; -; mRNA.
DR HSSP; P01869; 1A56.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 62.3%; Score 435.5; DB 2; Length 159;
Best Local Similarity 60.6%; Pred. No. 1.7e-36;
Matches 80; Conservative 22; Mismatches 25; Indels 5; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVWQMPGKGLWGMGIYPGSDTRY 60
DB 20 QQLVQSGAEVKKPGASVKSCKGSGYFTSYWIGVWQMPGKGLWGMVNPSCGARY 79
QY 61 SPSPQOQATISADKSI STAYLOWSLKASDTAMYYCARHVDV---GATIGGYYHYHGMND 117
DB 80 SOKFGRLTMTDSTSYVMDLSRLSDTAVYFCAREMEITFGGAVSKGFYY--GND 137
QY 118 VWGQTTTVSS 129
DB 138 VWGQTTTVSS 149

RESULT 3
Q921C4 MOUSE
ID Q921C4 MOUSE PRELIMINARY; PRT; 118 AA.
AC Q921C4;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Mattis L.A., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Mol. Immunol. 34:441-452(1997).
CC -----
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CC -----
DR EMBL; U78801; AAD00293.1; -; mRNA.
DR HSSP; P01751; 1NQB.
DR SMR; Q9Z1C4; 1-118.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EC559D31EC4FC CRC64;

Query Match 59.9%; Score 418.5; DB 2; Length 118;
Best Local Similarity 58.9%; Pred. No. 6.6e-35;
Matches 76; Conservative 23; Mismatches 19; Indels 11; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVWQMPGKGLWGMGIYPGSDTRY 60
DB 1 QVQVQSGAEALRPWASVKLSCKASGYNFNSQWVQKQRPQGQLEWIGAIYPGDTSY 60
QY 61 SPSPQOQATISADKSI STAYLOWSLKASDTAMYYCARHVDVVGATIGGYYHYHGMVWG 120
DB 61 TQKFRGKATLTADKSSSTAYMQLSLASEDSAVYYCARR-----TVGGYF-----DYWG 109
QY 121 QGTTTVSS 129
DB 110 QGTTTVSS 118

RESULT 4
Q3KQK2 MOUSE
ID Q3KQK2 MOUSE PRELIMINARY; PRT; 479 AA.
AC Q3KQK2;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 27-JUN-2006, entry version 8.
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
RC old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

```

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Straub L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitney M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months  
 RC old;  
 RG NTH MGC Project;  
 RL Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.  
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 CC -----  
 CC EMBL; BC106157; AAI06158.1; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.  
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.  
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_C1-set.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003599; Ig\_sub.  
 DR InterPro; IPR013106; Ig\_v-set.  
 DR InterPro; IPR003596; Ig\_v-set\_sub.  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS08335; IG-LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 DR KW Hypothetical protein; Immunoglobulin C region; Immunoglobulin domain;  
 KW Membrane; Repeat; Transmembrane.  
 SQ SEQUENCE 479 AA; 51745 MW; DB88E95F136BD78E CRC64;  
 Query Match 58.2%; Score 407; DB 2; Length 479;  
 Best Local Similarity 58.9%; Pred. No. 5.1e-33;  
 Matches 76; Conservative 20; Mismatches 19; Indels 14; Gaps 2;  
 QY 1 EVOLVSGAEVKKPGESLKISCKGSGYSFTSYWIGVWVRQMPGKLEWMIYPGDSDFY 60  
 Db 20 QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGVWVRQMPGKLEWMIYPGDSDFY 79  
 QY 61 SPSFQQAATISADKSIATYLOWSSLSKASDTAMYICARHVDVGATIGGYVYHGMVDWG 120  
 Db 80 SQKVGKATLTADKSSSTAYMQLSLASDSAVYICAR-----TFYP---DSWG 125  
 QY 121 QGTTVTSS 129  
 Db 126 QGTTLTSS 134  
 RESULT 5  
 Q65ZC8 HUMAN  
 ID Q65ZC8 HUMAN PRELIMINARY; PRT; 244 AA.  
 AC Q65ZC8;  
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.  
 DT 11-OCT-2004, sequence version 1.

DT 18-APR-2006, entry version 10.  
 DE Single-chain Fv (Fragment).  
 GN Name=scFv;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
 OC Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=9732799; PubMed=9219263; DOI=10.1038/nbt0797-629;  
 RA Kontermann R.E., Wing M.G., Winter G.;  
 RT "Complement recruitment using bispecific diabodies";  
 RL Nat. Biotechnol. 15:629-631(1997).  
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 CC -----  
 CC EMBL; Y13057; CAA73500.1; -; mRNA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003599; Ig\_sub.  
 DR InterPro; IPR013106; Ig\_v-set.  
 DR InterPro; IPR003596; Ig\_v-set\_sub.  
 DR Pfam; PF07686; V-set; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 2.  
 DR PROSITE; PS08335; IG-LIKE; 2.  
 KW Immunoglobulin domain.  
 FT NON\_TER 1 1  
 FT NON\_TER 244 244  
 SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;  
 Query Match 57.7%; Score 403; DB 2; Length 244;  
 Best Local Similarity 58.9%; Pred. No. 6e-33;  
 Matches 76; Conservative 23; Mismatches 22; Indels 8; Gaps 2;  
 QY 1 EVOLVSGAEVKKPGESLKISCKGSGYSFTSYWIGVWVRQMPGKLEWMIYPGDSDFY 60  
 Db 1 QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGVWVRQMPGKLEWMIYPGDSDFY 60  
 QY 61 SPSFQQAATISADKSIATYLOWSSLSKASDTAMYICARHVDVGATIGGYVYHGMVDWG 120  
 Db 61 AQRFQGRVTWTRDTSISAAVMEVSLRSDDTAVYICARE-GTGSAL-----YGMVDWG 112  
 QY 121 QGTTVTSS 129  
 Db 113 QGTLVTSS 121  
 RESULT 6  
 Q52L51 MOUSE  
 ID Q52L51 MOUSE PRELIMINARY; PRT; 483 AA.  
 AC Q52L51;  
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 24-MAY-2005, sequence version 1.  
 DT 27-JUN-2006, entry version 16.  
 DE LOC544903 protein.  
 GN Name=LOC544903;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months  
 RC old;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,



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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.A., Touchman J.W., Green E.D., Dickinson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor; WAP-TGF alpha model. 7 months
RC old;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC094065; AAH94065.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1-set.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003599; IG_sub.
DR InterPro; IPR013106; IG_V-set.
DR InterPro; IPR003596; IG_V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Immunoglobulin C region; Immunoglobulin domain; Membrane; Repeat;
KW Transmembrane.
SQ SEQUENCE 483 AA; 52167 MW; C0FDB9168795FEB4 CRC64;

Query Match 56.9%; Score 398; DB 2; Length 483;
Best Local Similarity 59.1%; Pred. No. 4.4e-32;
Matches 75; Conservative 20; Mismatches 22; Indels 10; Gaps 2;

QY 3 QLVSQAEVKKPGESLIKSGSYFTSYWIGVRQMPKGLWMMGIYPGDSITRYP 62
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
22 QLQSGAEVKKPGASVKISCKASGYAFSGPWNVYKQPKGLEWIGRIYPGDGETHYSG 81
QY 63 SFQQTATISADKSIATYALQWSLKSADPTAMYYCARHVDVGATIGYGYIYHGMVWGOG 122
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 QPKGRATLTADKSSSTAYVQLNGLTSDSAVYFCAR-----GNWPYVY--LDVWGAG 131

QY 123 TTVTVSS 129
Db |||:|||||
132 TTVTVSS 138

RESULT 7
Q7TMT6_MOUSE PRELIMINARY; PRT; 614 AA.
ID Q7TMT6_MOUSE
AC Q7TMT6;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 25-JUL-2006, entry version 31.
DE MGC60843 protein.

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GN Name=Igh-6; Synonyms=MGC60843;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RC Pubmed=12477932; DOI=10.1073/pnas.242603899;
RG Mammalian Gene Collection Program Team;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RG NIH MGC Project;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC053409; AAH53409.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR MGI; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B cell receptor complex; IEA.
DR GO; GO:0003897; C:external side of plasma membrane; IEA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IEA.
DR GO; GO:0048471; C:perinuclear region; IEA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:000187; P:activation of MAPK activity; IEA.
DR GO; GO:0030333; P:antigen processing; IEA.
DR GO; GO:0050853; P:B cell receptor signaling pathway; IEA.
DR GO; GO:045022; P:early endosome to late endosome transport; IEA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IEA.
DR GO; GO:0038890; P:positive regulation of B cell proliferation; IEA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IEA.
DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . . ; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1-set.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003599; IG_sub.
DR InterPro; IPR013106; IG_V-set.
DR InterPro; IPR003596; IG_V-set_sub.
DR Pfam; PF07654; C1-set; 4.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
KW Immunoglobulin C region; Immunoglobulin domain; Membrane; Repeat;
KW Transmembrane.

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CC -----
DR EMBL; BC098504; AAH98504.1; -; mRNA.
DR MGI; MGI:96448; Igh-6.
DR GO; GO:0019815; C:cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0000187; P:activation of MAPK activity; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0050853; P:B cell receptor signaling pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . ; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR Pfam; PF07654; C1-set; 4.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin C region; Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SQ SEQUENCE 617 AA; 68520 MW; BCF2AEC857CD3D12 CRC64;

Query Match 56.2%; Score 392.5; DB 2; Length 617;
Best Local Similarity 55.8%; Pred. No. 2.1e-31;
Matches 72; Conservative 23; Mismatches 27; Indels 7; Gaps 1;

QY 1 EVOLVSGAEVKKPGESLKISCKGSGYSTSYWIGVROMPGKLEWGMGIYPGDSDTRY 60
DB 20 QVQLQSGAEAKPGASVKLSCKASGYTFTSYWMMHWKORPGQGLEWIGTVNPSSGYTKY 79
QY 61 SPSPFQQAATISADKSIATYLOWSSLSKASDTAMYICARHVDVCGATGGYYHYHGMVDVG 120
DB 80 NQKFKDKATLTADKSSSTAYMQLSSLTYSVAVYICARR-----EGHLLWVYNDYWG 132
QY 121 QGTTVTSS 129
DB 133 QGTSVTSS 141

RESULT 10
Q9UL92 HUMAN PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Homidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9827139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.B., Kalis N.N., Berney S.M.,
RA Young D.C.;

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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CC -----
DR EMBL; AF035022; AAD56258.1; -; mRNA.
DR HSSP; P01751; INQB.
DR LinkHub; Q9UL92; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 56.0%; Score 391.5; DB 2; Length 124;
Best Local Similarity 58.0%; Pred. No. 4.2e-32;
Matches 76; Conservative 19; Mismatches 27; Indels 9; Gaps 2;

QY 1 EVOLVSGAEVKKPGESLKISCKGSGYSTSYWIGVROMPGKLEWGMGIYPGDSDTRY 60
DB 1 EVOLVESGAEVKKPGASVKRSKASGYTFTSYWMMHWKORPGQGLEWGMGIINPSGGTSY 60
QY 61 SPSPFQQAATISADKSIATYLOWSSLSKASDTAMYICARHVDVCGATGGYYHYHGMVDV 118
DB 61 AQKFGQGVTRTSTSTVYVMEUSSLRSEDATVYICARGLYVVVPAFSPR-----DY 113
QY 119 WGGTGVTVSS 129
DB 114 WGGTGLTVSS 124

RESULT 11
Q8VCX7 MOUSE PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 27-JUN-2006, entry version 33.
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 500 AA; 54154 MW; 0A5BFA43F2A3CC6D9 CRC64;

Query Match 55.9%; Score 390.5; DB 2; Length 500;
Best Local Similarity 56.9%; Pred. No. 2.7e-31;
Matches 74; Conservative 21; Mismatches 32; Indels 3; Gaps 2;

QY 1 EVQLVQSGAEVKPKGSLSKISCKGSGYSFTSYWIGVROMPGKGLWGMGIIPGDSSTRY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVQSGAEVMPGASVRKSTGTAFTHTYSIIWVROAPQGGLWGMWISFSSDSTRF 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SPFSFQQAATISADKSGISTAYLQWSSLSKASDTAMYICA-RHVDVGATIGGYGYYHYHGMVW 119
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AKKFGQGRVTLTDTSTSTVYMEISSLRSDDTAVYICAREYCSYSSQNDYIIYY--MDVW 137
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 GQTTVTVSS 129
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 138 GKGTTVTVSS 147
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
Q924P9 MOUSE
ID Q924P9_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q924P9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001; sequence version 1.
DT 18-APR-2006, entry version 19.
DE V303-D-J-C mu protein (fragment).
GN Name=V303-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95018269; PubMed=7523684;
RA Pokuluri P.R., Bouthillier P., Li Y., Kuderova A., Lee J., Cygler M.;
RT "Preparation, characterization and crystallization of an antibody Fab
RT fragment that recognizes RNA. Crystal structures of native Fab and
RT three Fab-monomononucleotide complexes.";
RL J. Mol. Biol. 243:283-297(1994).
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CC -----
DR EMBL; AB069916; BAB63932.1; -; mRNA.
DR PIR; PH1160; PH1160.
DR PIR; PH1161; PH1161.
DR PIR; PH1162; PH1162.
DR PIR; S53751; S53751.
DR HSSP; P01751; 1AGW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG sub.
DR InterPro; IPR013106; IG_V-set.
DR InterPro; IPR003596; IG_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 1
FT TER 143
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;

Query Match 55.7%; Score 389.5; DB 2; Length 143;
Best Local Similarity 56.6%; Pred. No. 8e-32;
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Matches 73; Conservative 19; Mismatches 26; Indels 11; Gaps 1;

QY 1 EVQLVQSGAEVKPKGSLSKISCKGSGYSFTSYWIGVROMPGKGLWGMGIIPGDSSTRY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVMPGASVKLSKASGYTFTSYWVQWVKQRPQGGLWGIIDPSDSYNY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SPFSFQQAATISADKSGISTAYLQWSSLSKASDTAMYICARHVDVGATIGGYGYYHYHGMVW 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKPKGKATLTVDTSSTAYMQLSSLTSEDASVYVCASH-----YIGSSSDVWG 109
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GQTTVTVSS 129
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 GQTTVTVSS 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
Q569W9 MOUSE
ID Q569W9_MOUSE PRELIMINARY; PRT; 468 AA.
AC Q569W9;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005; sequence version 1.
DT 27-JUN-2006, entry version 15.
DE Igh-1a protein.
GN Name=Igh-1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II; TISSUE=Mammary tumor metastasized to lung. Tumor
RC arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II; TISSUE=Mammary tumor metastasized to lung. Tumor
RC arose spontaneously;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; BC092271; AAH92271.1; -; mRNA.
DR SMR; Q569W9; 20-464.
DR MGI; MGI:96443; Igh-1a.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
```



GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:06:51 ; Search time 16 Seconds  
(without alignments)  
696.311 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EVOLVQSGAEVKKPGESLK1.....YYHHGMDVMGQGTIVTSS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PTUS\_COMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	82.7	119	2	US-09-025-769B-26
2	578	82.7	119	2	US-09-490-070A-26
3	578	82.7	119	2	US-09-490-153-26
4	578	82.7	119	2	US-09-490-324-26
5	571.5	81.8	120	2	US-09-025-769B-40
6	571.5	81.8	120	2	US-09-025-769B-67
7	571.5	81.8	120	2	US-09-490-070A-40
8	571.5	81.8	120	2	US-09-490-070A-67
9	571.5	81.8	120	2	US-09-490-153-40
10	571.5	81.8	120	2	US-09-490-153-67
11	571.5	81.8	120	2	US-09-490-324-40
12	571.5	81.8	120	2	US-09-490-324-67
13	519	74.2	98	1	US-08-665-202-33
14	519	74.2	98	1	US-09-315-574-33
15	519	74.2	98	2	US-10-194-975-45
16	519	74.2	117	2	US-08-545-809A-133
17	519	74.2	117	2	US-09-515-697-133
18	518	74.1	129	1	US-08-665-202-32
19	518	74.1	129	2	US-09-315-574-32
20	518	74.1	258	1	US-08-665-202-5
21	518	74.1	258	2	US-09-315-574-5
22	518	74.1	262	2	US-09-069-821-4
23	518	74.1	262	2	US-09-956-086-4
24	518	74.1	262	2	US-09-956-087-4
25	518	74.1	282	2	US-09-420-592A-7
26	518	74.1	282	2	US-09-985-442-7

Sequence 7, Appli  
Sequence 81, Appl  
Sequence 81, Appl  
Sequence 171, App  
Sequence 171, App  
Sequence 7, Appli  
Sequence 44, Appl  
Sequence 44, Appl  
Sequence 53, Appl  
Sequence 53, Appl  
Sequence 53, Appl  
Sequence 53, Appl  
Sequence 45, Appl  
Sequence 46, Appl  
Sequence 48, Appl  
Sequence 55, Appl  
Sequence 45, Appl  
Sequence 46, Appl  
Sequence 48, Appl

#### ALIGNMENTS

RESULT 1  
US-09-025-769B-26  
; Sequence 26, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-26  
Query Match 82.7%; Score 578; DB 2; Length 119;  
Best Local Similarity 87.6%; Pred. No. 6.5e-48;

Matches 113; Conservative 2; Mismatches 4; Indels 10; Gaps 3;  
QY 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60  
DB 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60  
QY 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120  
DB 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120  
QY 121 QGTLTVTSS 129  
DB 111 QGTLTVTSS 119

## RESULT 2

US-09-490-070A-26  
; Sequence 26, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; White & McAuliffe  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,070A  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Colin G. Sandercock, Esq.  
; REGISTRATION NUMBER: 37629-0005  
; REFERENCE/DOCKET NUMBER: 37629-0005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 912-2000  
; TELEFAX: (202) 912-2020  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-490-070A-26  
Query Match 82.7%; Score 578; DB 2; Length 119;  
Best Local Similarity 87.6%; Pred. No. 6.5e-48;  
Matches 113; Conservative 2; Mismatches 4; Indels 10; Gaps 3;  
QY 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60  
DB 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60  
QY 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120  
DB 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120  
QY 121 QGTLTVTSS 129  
DB 111 QGTLTVTSS 119

DB 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 110  
QY 121 QGTLTVTSS 129  
DB 111 QGTLTVTSS 119  
RESULT 3  
US-09-490-153-26  
; Sequence 26, Application US/09490153  
; Patent No. 6706484  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,153  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-490-153-26  
Query Match 82.7%; Score 578; DB 2; Length 119;  
Best Local Similarity 87.6%; Pred. No. 6.5e-48;  
Matches 113; Conservative 2; Mismatches 4; Indels 10; Gaps 3;  
QY 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60  
DB 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60  
QY 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120  
DB 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120  
QY 121 QGTLTVTSS 129  
DB 111 QGTLTVTSS 119



## RESULT 4

US-09-490-324-26  
; Sequence 26, Application US/09490324  
; Patent No. 6828422

## GENERAL INFORMATION:

APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324  
; FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769  
; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-490-324-26

Query Match 82.7%; Score 578; DB 2; Length 119;  
Best Local Similarity 87.6%; Pred. No. 6.5e-48;  
Matches 113; Conservative 2; Mismatches 4; Indels 10; Gaps 3;

Qy 1 EVLVQSGAEVKPGESLKIICKSGSGYSFTSYWIGWVRQMPGKLEWMGIIPGDSSTRY 60  
Db 1 EVLVQSGAEVKPGESLKIICKSGSGYSFTSYWIGWVRQMPGKLEWMGIIPGDSSTRY 60

Qy 61 SPSFGQATISADKISITAYLQWSSLKASDTAMYCARHVDVGATIGGYYYHYHGMVWG 120  
Db 61 SPSFGQVITISADKISITAYLQWSSLKASDTAMYCARHVDVGATIGGYYYHYHGMVWG 110

Qy 121 QGTTVTSS 129

Db 111 QGTLVTSS 119

## RESULT 5

US-09-025-769B-40

; Sequence 40, Application US/09025769B  
; Patent No. 6300064

## GENERAL INFORMATION:

APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-40

Query Match 81.8%; Score 571.5; DB 2; Length 120;  
Best Local Similarity 86.8%; Pred. No. 2.7e-47;  
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

Qy 1 EVLVQSGAEVKPGESLKIICKSGSGYSFTSYWIGWVRQMPGKLEWMGIIPGDSSTRY 60  
Db 1 EVLVQSGAEVKPGESLKIICKSGSGYSFTSYWIGWVRQMPGKLEWMGIIPGDSSTRY 60

Qy 61 SPSFGQATISADKISITAYLQWSSLKASDTAMYCARHVDVGATIGGYYYHYHGMVWG 120  
Db 61 SPSFGQVITISADKISITAYLQWSSLKASDTAMYCARHVDVGATIGGYYYHYHGMVWG 111

Qy 121 QGTTVTSS 129

Db 112 QGTLVTSS 120

## RESULT 6

US-09-025-769B-67

; Sequence 67, Application US/09025769B  
; Patent No. 6300064

## GENERAL INFORMATION:

APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
;; STREET: 1251 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10021

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/025,769B  
;; FILING DATE: 18-FEB-1998

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 95 11 3021.0  
;; FILING DATE: 18-AUG-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: James F. Haley, Jr., Esq.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: MORPHO/5  
;; TELEPHONE: (212)596-9000  
;; TELEFAX: (212)596-9090

;; INFORMATION FOR SEQ ID NO: 67:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 120 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein

US-09-025-769B-67

Query Match 81.8%; Score 571.5; DB 2; Length 120;  
Best Local Similarity 86.8%; Pred. No. 2.7e-47;  
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;  
  
QY 1 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVROMPGKLEWNGIIPGSDSTRY 60  
DB 1 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVROMPGKLEWNGIIPGSDSTRY 60  
  
QY 61 SPSPGQQTISADKSGISTAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120  
DB 61 SPSPGQQTISADKSGISTAYLQWSSLKASDTAMYCARW-----GGDGFY--AMDYWG 111

QY 121 QGTTVTSS 129  
DB 112 QGTLTVSS 120

#### RESULT 7

US-09-490-070A-40  
; Sequence 40, Application US/09490070A  
; Patent No. 6696248

#### GENERAL INFORMATION:

APPLICANT: Knappik, Achim

;; Pack, Peter  
;; Ilag, Vic  
;; Ge, Liming  
;; Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/490,070A

;; FILING DATE: 24-Jan-2000

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: EP 95 11 3021.0

;; FILING DATE: 18-AUG-1995

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Colin G. Sandercock, Esq.

;; REGISTRATION NUMBER: 31,298

;; REFERENCE/DOCKET NUMBER: 37629-0005

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (202) 912-2000

;; TELEFAX: (202) 912-2020

;; INFORMATION FOR SEQ ID NO: 40:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 120 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: <Unknown>

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-490-070A-40

Query Match 81.8%; Score 571.5; DB 2; Length 120;  
Best Local Similarity 86.8%; Pred. No. 2.7e-47;  
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVROMPGKLEWNGIIPGSDSTRY 60  
DB 1 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVROMPGKLEWNGIIPGSDSTRY 60

QY 61 SPSPGQQTISADKSGISTAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120  
DB 61 SPSPGQQTISADKSGISTAYLQWSSLKASDTAMYCARW-----GGDGFY--AMDYWG 111

QY 121 QGTTVTSS 129  
DB 112 QGTLTVSS 120

#### RESULT 8

US-09-490-070A-67

; Sequence 67, Application US/09490070A

; Patent No. 6696248

;; GENERAL INFORMATION:

APPLICANT: Knappik, Achim

;; Pack, Peter

;; Ilag, Vic

;; Ge, Liming

;; Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-070A-67

Query Match      81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVLVOSGAEVKKPGESLKISKCKSGSYFTSYWIGVROMPGKLEWNGIIPGSDTRY 60
Db 1 EVLVOSGAEVKKPGESLKISKCKSGSYFTSYWIGVROMPGKLEWNGIIPGSDTRY 60
QY 61 SPSFQQTATISADKSIISTAYLOWSSLKASDTAMYICARHVDVGATIGGYIYYHGMVDWG 120
Db 61 SPSFQQTATISADKSIISTAYLOWSSLKASDTAMYICARHVDVGATIGGYIYYHGMVDWG 120
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 9
US-09-490-153-40
; Sequence 40, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid

; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-40

Query Match      81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVLVOSGAEVKKPGESLKISKCKSGSYFTSYWIGVROMPGKLEWNGIIPGSDTRY 60
Db 1 EVLVOSGAEVKKPGESLKISKCKSGSYFTSYWIGVROMPGKLEWNGIIPGSDTRY 60
QY 61 SPSFQQTATISADKSIISTAYLOWSSLKASDTAMYICARHVDVGATIGGYIYYHGMVDWG 120
Db 61 SPSFQQTATISADKSIISTAYLOWSSLKASDTAMYICARHVDVGATIGGYIYYHGMVDWG 120
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 10
US-09-490-153-67
; Sequence 67, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-67

Query Match      81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGVROMPGKLEWMGIIYPGDSSTRY 60
Db 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGVROMPGKLEWMGIIYPGDSSTRY 60
QY 61 SPSPGQQTISADKSIKSKSGSYFTSYWIGVROMPGKLEWMGIIYPGDSSTRY 120
Db 61 SPSPGQQTISADKSIKSKSGSYFTSYWIGVROMPGKLEWMGIIYPGDSSTRY 120
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 11
US-09-490-324-40
; Sequence 40, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-324-40

Query Match      81.8%; Score 571.5; DB 2; Length 120;
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Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGVROMPGKLEWMGIIYPGDSSTRY 60
Db 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGVROMPGKLEWMGIIYPGDSSTRY 60
QY 61 SPSPGQQTISADKSIKSKSGSYFTSYWIGVROMPGKLEWMGIIYPGDSSTRY 120
Db 61 SPSPGQQTISADKSIKSKSGSYFTSYWIGVROMPGKLEWMGIIYPGDSSTRY 120
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 12
US-09-490-324-67
; Sequence 67, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-324-67

Query Match      81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGVROMPGKLEWMGIIYPGDSSTRY 60
Db 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGVROMPGKLEWMGIIYPGDSSTRY 60
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QY 61 SPSFQOATISADKSISTAYLOWSSLSKASDTAMYCARHVDVCATIGGGYIIYHGMVWG 120  
DB 61 SPSFQOQVTISADKSISTAYLOWSSLSKASDTAMYCARW-----GGDGFY--AMDYWG 111  
QY 121 QGTTVTVSS 129  
DB 112 QGTLVTVSS 120

RESULT 13  
US-08-665-202-33  
; Sequence 33, Application US/08665202  
; Patent No. 5977322  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,202  
; FILING DATE: 13-JUN-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,238  
; FILING DATE: 14-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,250  
; FILING DATE: 15-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 02307E-061410  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-665-202-33

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Best Local Similarity 99.0%; Pred. No. 2.3e-42;  
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVRQMPGKGLWNGIIPGSDTRY 60  
DB 1 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVRQMPGKGLWNGIIPGSDTRY 60  
QY 61 SPSFQOATISADKSISTAYLOWSSLSKASDTAMYCAR 98  
DB 61 SPSFQOQVTISADKSISTAYLOWSSLSKASDTAMYCAR 98

RESULT 14  
US-09-315-574-33  
; Sequence 33, Application US/09315574

; Patent No. 6512097  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.  
; STREET: Four Embarcadero Center, Suite 1100  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4106  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/315,574  
; FILING DATE: 20-MAY-99  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,238  
; FILING DATE: 14-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,250  
; FILING DATE: 15-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/665,202  
; FILING DATE: 13-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 02307E-061411  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-315-574-33

Query Match 74.2%; Score 519; DB 2; Length 98;  
Best Local Similarity 99.0%; Pred. No. 2.3e-42;  
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVRQMPGKGLWNGIIPGSDTRY 60  
DB 1 EVLVQSGAEVKKPGESLKISCKSGSYFTSYWIGVRQMPGKGLWNGIIPGSDTRY 60  
QY 61 SPSFQOATISADKSISTAYLOWSSLSKASDTAMYCAR 98  
DB 61 SPSFQOQVTISADKSISTAYLOWSSLSKASDTAMYCAR 98

RESULT 15  
US-10-194-975-45  
; Sequence 45, Application US/10194975  
; Patent No. 6881557  
; GENERAL INFORMATION:  
; APPLICANT: Foote, Jefferson  
; TITLE OF INVENTION: Super Humanized Antibodies  
; FILE REFERENCE: 501231.01  
; CURRENT APPLICATION NUMBER: US/10/194,975  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12

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; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-45

Query Match      74.2%; Score 519; DB 2; Length 98;
Best Local Similarity 99.0%; Pred. No. 2.3e-42;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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   |||||
Db 1 EVQLVQSGAEVKKPGESLKISCKSGSYFTSYWIGWVRQMPGKLEWMGIIYPGDSITRY 60
   |||||

Qy 61 SPSFQQTISADKSIISTAYLQWSSLKASDTAMYICAR 98
   |||||
Db 61 SPSFQQTISADKSIISTAYLQWSSLKASDTAMYICAR 98
   |||||

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Search completed: April 25, 2007, 04:08:30  
Job time : 17.2161 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 48 Seconds  
(without alignments)  
1251.741 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EVLVQSGAEVKKPGESLK1.....YYYYHGMVWGQTTVTSS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_Main:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	699	100.0	129	4	US-10-041-860-29
2	699	100.0	129	4	US-10-041-860-215
3	699	100.0	129	4	US-10-041-860-250
4	699	100.0	129	4	US-10-041-860-319
5	699	100.0	129	4	US-10-041-860-319
6	603	86.3	125	5	US-10-665-383-38
7	598.5	85.6	126	4	US-10-041-860-313
8	593.5	84.9	126	4	US-10-041-860-27
9	593.5	84.9	126	4	US-10-041-860-214
10	593.5	84.9	126	4	US-10-041-860-249
11	593.5	84.9	126	4	US-10-665-383-34
12	592.5	84.8	126	4	US-10-041-860-23
13	592.5	84.8	126	4	US-10-041-860-248
14	592.5	84.8	126	4	US-10-041-860-300
15	592.5	84.8	126	4	US-10-665-383-26
16	590	84.4	118	5	US-10-726-332-143
17	589.5	84.3	126	4	US-10-041-860-35
18	589.5	84.3	126	4	US-10-041-860-216
19	589.5	84.3	126	4	US-10-041-860-251
20	589.5	84.3	126	4	US-10-041-860-337
21	589.5	84.3	126	4	US-10-665-383-50
22	587	84.0	118	5	US-10-726-332-3
23	585	83.7	118	5	US-10-726-332-139
24	584	83.5	118	5	US-10-726-332-13
25	584	83.5	118	5	US-10-726-332-140
26	580	83.0	118	5	US-10-726-332-29
27	578	82.7	119	5	US-10-834-397-26

28	576.5	82.5	226	4	US-10-128-520-159	Sequence 159, App
29	576	82.4	252	3	US-09-880-748-1537	Sequence 1537, App
30	576	82.4	252	4	US-10-283-418-1537	Sequence 1537, App
31	576	82.4	252	6	US-11-054-515-1537	Sequence 1537, App
32	576	82.4	252	6	US-11-266-444-1537	Sequence 1537, App
33	573.5	82.0	224	4	US-10-128-520-180	Sequence 180, App
34	573	82.0	118	5	US-10-726-332-145	Sequence 145, App
35	572.5	81.9	116	5	US-10-727-155-100	Sequence 100, App
36	572.5	81.9	222	4	US-10-128-520-169	Sequence 169, App
37	571.5	81.8	120	4	US-10-125-687-6	Sequence 6, Appli
38	571.5	81.8	120	5	US-10-996-191-6	Sequence 6, Appli
39	571.5	81.8	120	5	US-10-834-397-40	Sequence 40, Appl
40	571.5	81.8	120	5	US-10-834-397-67	Sequence 67, Appl
41	571.5	81.8	126	4	US-10-041-860-46	Sequence 46, Appl
42	571.5	81.8	126	4	US-10-041-860-217	Sequence 217, App
43	571.5	81.8	126	4	US-10-041-860-366	Sequence 366, App
44	571.5	81.8	126	4	US-10-655-383-70	Sequence 70, Appl
45	569.5	81.5	224	4	US-10-128-520-165	Sequence 165, App

## ALIGNMENTS

RESULT 1  
US-10-041-860-29  
; Sequence 29, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Peng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: ARGENIX.051A  
; CURRENT APPLICATION NUMBER: US/10/041.860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-29

Query Match 100.0%; Score 699; DB 4; Length 129;  
Best Local Similarity 100.0%; Pred. No. 2.4e-55;  
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGVROMPKGLEWNGIYPGSDTRY 60  
DB 1 EVLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGVROMPKGLEWNGIYPGSDTRY 60

QY 61 SPSPFQQTATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYYYYHGMVWG 120  
DB 61 SPSPFQQTATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYYYYHGMVWG 120

QY 121 QGTTVTSS 129  
DB 121 QGTTVTSS 129

RESULT 2  
US-10-041-860-215  
; Sequence 215, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi

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; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-215

Query Match      100.0%; Score 699; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWGMGIYPGDSSTRY 60
DB 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWGMGIYPGDSSTRY 60
QY 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
DB 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
QY 121 QGTTVTVSS 129
DB 121 QGTTVTVSS 129

RESULT 3
US-10-041-860-250
; Sequence 250, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-250

Query Match      100.0%; Score 699; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWGMGIYPGDSSTRY 60
DB 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWGMGIYPGDSSTRY 60
QY 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
DB 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
QY 121 QGTTVTVSS 129
DB 121 QGTTVTVSS 129

RESULT 4
US-10-041-860-319
; Sequence 319, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-319

Query Match      100.0%; Score 699; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWGMGIYPGDSSTRY 60
DB 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWGMGIYPGDSSTRY 60
QY 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
DB 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
QY 121 QGTTVTVSS 129
DB 121 QGTTVTVSS 129

RESULT 5
US-10-665-383-38
; Sequence 38, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-38
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Query Match      100.0%; Score 699; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVQSGAEVKKPGESLKISCKSGYSFTSYWIGWVRQMPGKLEWMGIIYPGDSSTRY 60
DB 1 EVOLVQSGAEVKKPGESLKISCKSGYSFTSYWIGWVRQMPGKLEWMGIIYPGDSSTRY 60

QY 61 SPFSQOQTISADKSI STAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120
DB 61 SPFSQOQTISADKSI STAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120

QY 121 QGTTVTSS 129
DB 121 QGTTVTSS 129

RESULT 6
US-10-891-658-79
; Sequence 79, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; PRIOR FILING DATE: 2004-07-15
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-79

Query Match      86.3%; Score 603; DB 5; Length 125;
Best Local Similarity 88.4%; Pred. No. 1.1e-46;
Matches 114; Conservative 7; Mismatches 4; Indels 4; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKSGYSFTSYWIGWVRQMPGKLEWMGIIYPGDSSTRY 60
DB 1 EVOLVQSGAEVKKPGESLKISCKSGYNFTTYWIGWVRQMPGKLEWMGIIYPGDSSTRY 60

QY 61 SPFSQOQTISADKSI STAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120
DB 61 SPFSQOQTISADKSI STAYLQWSSLSKASDTAMYCARNY-YGS---GYYYYYGNVWG 116

QY 121 QGTTVTSS 129
DB 117 QGTTVTSS 125

RESULT 7
US-10-041-860-313
; Sequence 313, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
```

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; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-313

Query Match      85.6%; Score 598.5; DB 4; Length 126;
Best Local Similarity 86.5%; Pred. No. 2.8e-46;
Matches 115; Conservative 1; Mismatches 6; Indels 11; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKSGYSFTSYWIGWVRQMPGKLEWMGIIYPGDSSTRY 60
DB 1 EVOLVQSGAEVKKPGESLKISCKSGYSFTSYWIGWVRQMPGKLEWMGIIYPGDSSTRY 60

QY 61 SPFSQOQTISADKSI STAYLQWSSLSKASDTAMYCARHVDVGATIGGYY---YHGM 116
DB 61 SPFSQOQTISADKSI STAYLQWSSLSKASDTAMYCARH-----GSYYYGSETYYNVF 113

QY 117 DVWGQGTTLTVSS 129
DB 114 DYWGQGTTLTVSS 126

RESULT 8
US-10-041-860-27
; Sequence 27, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao-Dong
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-27

Query Match      84.9%; Score 593.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 7.8e-46;
Matches 114; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKSGYSFTSYWIGWVRQMPGKLEWMGIIYPGDSSTRY 60
DB 1 EVOLVQSGAEVKKPGESLKISCKSGYRFTSYWIGWVRQMPGKLEWMGIIYPGDSSTRY 60

QY 61 SPFSQOQTISADKSI STAYLQWSSLSKASDTAMYCARHVDVGATIGGYY---YHGM 116
DB 61 SPFSQOQTISADKSI STAYLQWSSLSKASDTAMYCARH-----GSYYYGSETYYNVF 113

QY 117 DVWGQGTTLTVSS 129
DB 114 DYWGQGTTLTVSS 126
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RESULT 9
US-10-041-860-214
; Sequence 214, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-214

Query Match      84.9%; Score 593.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 7.8e-46;
Matches 114; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

QY      1 EVQLVQSGAEVKPGESLKISCKGSGYFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60
Db      1 EVQLVQSGAEVKPGESLKISCKGSGYFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60

QY      61 SPSFQCGQTISADKSIATAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116
Db      61 SPSFQCGQTISADKSIATAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116

QY      117 DWGQGTTVTSS 129
Db      114 DWGQGTLVTSS 126

RESULT 11
US-10-665-383-34
; Sequence 34, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Jueigen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: Larochele, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-34

Query Match      84.9%; Score 593.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 7.8e-46;
Matches 114; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

QY      1 EVQLVQSGAEVKPGESLKISCKGSGYFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60
Db      1 EVQLVQSGAEVKPGESLKISCKGSGYFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60

QY      61 SPSFQCGQTISADKSIATAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116
Db      61 SPSFQCGQTISADKSIATAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116

QY      117 DWGQGTTVTSS 129
Db      114 DWGQGTLVTSS 126

RESULT 12
US-10-041-860-23
; Sequence 23, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-249

Query Match      84.9%; Score 593.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 7.8e-46;
Matches 114; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

QY      1 EVQLVQSGAEVKPGESLKISCKGSGYFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60
Db      1 EVQLVQSGAEVKPGESLKISCKGSGYFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60

QY      61 SPSFQCGQTISADKSIATAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116
Db      61 SPSFQCGQTISADKSIATAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116

QY      117 DWGQGTTVTSS 129
Db      114 DWGQGTLVTSS 126

RESULT 13
US-10-041-860-249
; Sequence 249, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-249

Query Match      84.9%; Score 593.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 7.8e-46;
Matches 114; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

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; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-23

Query Match      84.8%; Score 592.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 9.7e-46;
Matches 114; Conservative 2; Mismatches 6; Indels 11; Gaps 2;

Qy 1 EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLWMGIIYPGDSSTRY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLWMGIIYPGDSSTRY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGGYY----YHGM 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGGYY----YHGM 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 117 DVMGGTTLTVSS 129
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114 DVMGGTTLTVSS 126

RESULT 13
US-10-041-860-248
; Sequence 248, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 248
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-248

Query Match      84.8%; Score 592.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 9.7e-46;
Matches 114; Conservative 2; Mismatches 6; Indels 11; Gaps 2;

Qy 1 EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLWMGIIYPGDSSTRY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLWMGIIYPGDSSTRY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGGYY----YHGM 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGGYY----YHGM 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 117 DVMGGTTLTVSS 129
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114 DVMGGTTLTVSS 126

RESULT 14
US-10-041-860-300
; Sequence 300, Application US/10041860
; Publication No. US20030157109A1
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; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-300

Query Match      84.8%; Score 592.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 9.7e-46;
Matches 114; Conservative 2; Mismatches 6; Indels 11; Gaps 2;

Qy 1 EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLWMGIIYPGDSSTRY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLWMGIIYPGDSSTRY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGGYY----YHGM 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGGYY----YHGM 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 117 DVMGGTTLTVSS 129
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114 DVMGGTTLTVSS 126

RESULT 15
US-10-665-383-26
; Sequence 26, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-665-383-26

Query Match      84.8%; Score 592.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 9.7e-46;
Matches 114; Conservative 2; Mismatches 6; Indels 11; Gaps 2;

Qy 1 EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLWMGIIYPGDSSTRY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLWMGIIYPGDSSTRY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGGYY----YHGM 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGGYY----YHGM 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 61 SPSFOGVTISADKISTAYLOWSSLKASDTAMYCARHV-----SYVVSGSYNVF 113  
Qy 117 DVMGOGTTVTSS 129  
Db 114 DVMGOGTLVTSS 126

Search completed: April 25, 2007, 04:22:49  
Job time : 48.7373 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 04:23:02 ; Search time 50 Seconds  
(without alignments)  
533.620 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EVOLVQSGAEVKPGESLKI.....YYYYHGMVMDVGGQTTVTSS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 947558 seqs, 205760075 residues

Total number of hits satisfying chosen parameters: 947558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New.\*

- 1: /EMC Celerra\_SID33/ptodata/1/pubpaa/US08 NEW PUB.pbp.\*
- 2: /EMC Celerra\_SID33/ptodata/1/pubpaa/US06 NEW PUB.pbp.\*
- 3: /EMC Celerra\_SID33/ptodata/1/pubpaa/US07 NEW PUB.pbp.\*
- 4: /EMC Celerra\_SID33/ptodata/1/pubpaa/PTCT\_NEW PUB.pbp.\*
- 5: /EMC Celerra\_SID33/ptodata/1/pubpaa/US09 NEW PUB.pbp.\*
- 6: /EMC Celerra\_SID33/ptodata/1/pubpaa/US10 NEW PUB.pbp.\*
- 7: /EMC Celerra\_SID33/ptodata/1/pubpaa/US11 NEW PUB.pbp.\*
- 8: /EMC Celerra\_SID33/ptodata/1/pubpaa/US60\_NEW PUB.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	699	100.0	129	7	US-11-109-181-29
2	699	100.0	129	7	US-11-109-181-215
3	699	100.0	129	7	US-11-109-181-250
4	699	100.0	129	7	US-11-109-181-319
5	614	87.8	121	7	US-11-440-728-10
6	613.5	87.8	118	7	US-11-440-728-143
7	608	87.0	121	7	US-11-440-728-22
8	608	87.0	121	7	US-11-440-728-145
9	607	86.8	121	7	US-11-440-728-18
10	602	86.1	121	7	US-11-440-728-106
11	602	86.1	121	7	US-11-440-728-118
12	599	85.7	121	7	US-11-440-728-90
13	598.5	85.6	126	7	US-11-109-181-313
14	598	85.6	119	7	US-11-440-728-146
15	598	85.6	121	7	US-11-440-728-98
16	597.5	85.5	124	7	US-11-440-728-6
17	597	85.4	121	7	US-11-440-728-130
18	596	85.3	121	7	US-11-440-728-38
19	595.5	85.2	122	7	US-11-440-728-46
20	595	85.1	121	7	US-11-440-728-151
21	594	85.0	121	7	US-11-440-728-74
22	593.5	84.9	126	7	US-11-109-181-27
23	593.5	84.9	126	7	US-11-109-181-214
24	593.5	84.9	126	7	US-11-109-181-249
25	592.5	84.8	126	7	US-11-109-181-23

```

26 592.5 84.8 126 7 US-11-109-181-248 Sequence 248, App
27 592.5 84.8 126 7 US-11-109-181-300 Sequence 300, App
28 592 84.7 121 7 US-11-440-728-122 Sequence 122, App
29 592 84.7 156 7 US-11-396-178-170 Sequence 170, App
30 592 84.7 156 7 US-11-396-178-175 Sequence 175, App
31 592 84.7 182 7 US-11-396-178-100 Sequence 100, App
32 592 84.7 182 7 US-11-396-178-157 Sequence 157, App
33 590 84.4 121 7 US-11-440-728-58 Sequence 58, App
34 590 84.4 121 7 US-11-440-728-94 Sequence 94, App
35 590 84.4 178 7 US-11-396-178-92 Sequence 92, App
36 590 84.4 178 7 US-11-396-178-153 Sequence 153, App
37 589.5 84.3 126 7 US-11-109-181-35 Sequence 35, App
38 589.5 84.3 126 7 US-11-109-181-216 Sequence 216, App
39 589.5 84.3 126 7 US-11-109-181-251 Sequence 251, App
40 589.5 84.3 126 7 US-11-109-181-337 Sequence 337, App
41 588 84.1 121 7 US-11-440-728-102 Sequence 102, App
42 587 84.0 121 7 US-11-440-728-126 Sequence 126, App
43 585.5 83.8 122 7 US-11-440-728-42 Sequence 42, App
44 584.5 83.6 122 7 US-11-440-728-50 Sequence 50, App
45 579 82.8 121 7 US-11-440-728-34 Sequence 34, App

```

#### ALIGNMENTS

```

RESULT 1
US-11-109-181-29
; Sequence 29, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Biyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18.
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-29

```

```

Query Match 100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 EVOLVQSGAEVKPGESLKI...CKSGYSFTSYWIGVWRQMPGKGLWMMGIIYPGSDTRY 60
Db 1 EVOLVQSGAEVKPGESLKI...CKSGYSFTSYWIGVWRQMPGKGLWMMGIIYPGSDTRY 60
Qy 61 SPFSQOATISADKSI...TAYLQWSSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMVWG 120
Db 61 SPFSQOATISADKSI...TAYLQWSSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMVWG 120
Qy 121 QGTTVTVSS 129
Db 121 QGTTVTVSS 129

```

```

RESULT 2
US-11-109-181-215
; Sequence 215, Application US/11109181

```

```
Publication No. US20060293506A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT FILING DATE: US/11/109,181
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2005-04-18
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 215
LENGTH: 129
TYPE: PRT
ORGANISM: homo sapiens
US-11-109-181-215

Query Match      100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVLVQSGAEVKKPGESLKIACKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDSSTRY 60
Db      1 EVLVQSGAEVKKPGESLKIACKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDSSTRY 60

QY      61 SPSFQOATISADKSIATAYLQWSSLKASDTAMYYCARHVDVGATIGGYYHYHGMVDWG 120
Db      61 SPSFQOATISADKSIATAYLQWSSLKASDTAMYYCARHVDVGATIGGYYHYHGMVDWG 120

QY      121 QGTTVTVSS 129
Db      121 QGTTVTVSS 129

RESULT 4
US-11-109-181-319
Sequence 319, Application US/11109181
Publication No. US20060293506A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT FILING DATE: US/11/109,181
CURRENT APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 319
LENGTH: 129
TYPE: PRT
ORGANISM: homo sapiens
US-11-109-181-319

Query Match      100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVLVQSGAEVKKPGESLKIACKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDSSTRY 60
Db      1 EVLVQSGAEVKKPGESLKIACKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDSSTRY 60

QY      61 SPSFQOATISADKSIATAYLQWSSLKASDTAMYYCARHVDVGATIGGYYHYHGMVDWG 120
Db      61 SPSFQOATISADKSIATAYLQWSSLKASDTAMYYCARHVDVGATIGGYYHYHGMVDWG 120

QY      121 QGTTVTVSS 129
Db      121 QGTTVTVSS 129

RESULT 5
US-11-440-728-10
Sequence 10, Application US/11440728
Publication No. US20070014720A1
GENERAL INFORMATION:
APPLICANT: GAZIT-BORNSTEIN, Gadi
APPLICANT: GREEN, Larry L.
APPLICANT: YANG, Xiaodong
APPLICANT: QUEVA, Christophe
APPLICANT: BLAKE, David Charles
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
FILE REFERENCE: ABXAZ.003A
CURRENT APPLICATION NUMBER: US/11/440,728
```

```
; CURRENT FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-10

Query Match      87.8%; Score 614; DB 7; Length 121;
Best Local Similarity 89.9%; Pred. No. 8.5e-50;
Matches 116; Conservative 2; Mismatches 3; Indels 8; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWMMGLIYPGDS DTRY 60
   |||||
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWMMGLIYPGDS DTRY 60
   |||||

QY 61 SPSFQOQTISADKSI STAYLOWSSLKASDTAMYCARHVDVGATIGGYYHHGMDVWG 120
   |||||
Db 61 SPSFQOQTISADKSI STAYLOWSSLKASDTAMYCARHVDVGATIGGYYHHGMDVWG 120
   |||||

QY 121 QGTTVTSS 129
   |||||
Db 113 QGTTVTSS 121

RESULT 6
US-11-440-728-143
; Sequence 143, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-143

Query Match      87.8%; Score 613.5; DB 7; Length 118;
Best Local Similarity 89.9%; Pred. No. 9.3e-50;
Matches 116; Conservative 1; Mismatches 1; Indels 11; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWMMGLIYPGDS DTRY 60
   |||||
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWMMGLIYPGDS DTRY 60
   |||||

QY 61 SPSFQOQTISADKSI STAYLOWSSLKASDTAMYCARHVDVGATIGGYYHHGMDVWG 120
   |||||
Db 61 SPSFQOQTISADKSI STAYLOWSSLKASDTAMYCARHVDVGATIGGYYHHGMDVWG 120
   |||||

QY 121 QGTTVTSS 129
   |||||
Db 110 QGTTVTSS 118

RESULT 7
US-11-440-728-22
; Sequence 22, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-143

Query Match      87.8%; Score 613.5; DB 7; Length 118;
Best Local Similarity 89.9%; Pred. No. 9.3e-50;
Matches 116; Conservative 1; Mismatches 1; Indels 11; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWMMGLIYPGDS DTRY 60
   |||||
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWMMGLIYPGDS DTRY 60
   |||||

QY 61 SPSFQOQTISADKSI STAYLOWSSLKASDTAMYCARHVDVGATIGGYYHHGMDVWG 120
   |||||
Db 61 SPSFQOQTISADKSI STAYLOWSSLKASDTAMYCARHVDVGATIGGYYHHGMDVWG 120
   |||||

QY 121 QGTTVTSS 129
   |||||
Db 110 QGTTVTSS 118

RESULT 8
US-11-440-728-145
; Sequence 145, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-145

Query Match      87.0%; Score 608; DB 7; Length 121;
Best Local Similarity 91.5%; Pred. No. 3.1e-49;
Matches 118; Conservative 1; Mismatches 2; Indels 8; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWMMGLIYPGDS DTRY 60
   |||||
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWMMGLIYPGDS DTRY 60
   |||||

QY 61 SPSFQOQTISADKSI STAYLOWSSLKASDTAMYCARHVDVGATIGGYYHHGMDVWG 120
   |||||
Db 61 SPSFQOQTISADKSI STAYLOWSSLKASDTAMYCARHVDVGATIGGYYHHGMDVWG 120
   |||||

QY 121 QGTTVTSS 129
   |||||
Db 113 QGTTVTSS 121

RESULT 9
US-11-440-728-146
; Sequence 146, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-146

Query Match      87.0%; Score 608; DB 7; Length 121;
Best Local Similarity 91.5%; Pred. No. 3.1e-49;
Matches 118; Conservative 1; Mismatches 2; Indels 8; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWMMGLIYPGDS DTRY 60
   |||||
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWMMGLIYPGDS DTRY 60
   |||||

QY 61 SPSFQOQTISADKSI STAYLOWSSLKASDTAMYCARHVDVGATIGGYYHHGMDVWG 120
   |||||
Db 61 SPSFQOQTISADKSI STAYLOWSSLKASDTAMYCARHVDVGATIGGYYHHGMDVWG 120
   |||||

QY 121 QGTTVTSS 129
   |||||
Db 113 QGTTVTSS 121
```

Db	61	S P S F Q G V T I S A D K S I S T A Y L Q W S L X S A D T A M Y C A R	---V G A T-----N T Y Y G D M V N G 112
Qy	121	Q G T I V T V T S S	129
Db	113	O G T I V T V T S S	121

## RESULT 9

```

US-11-440-728-18
; Sequence 18, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-18

```

RESIT.T 10

```

US-11-440-728-106
; Sequence 106, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/6886,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-11-440-728-106

Query Match	86.1%;	Score 502;	DB 7;	Length 121;
Best Local Similarity	89.8%;	Pred. No. 1.1e-48;		
Matches 115;	Conservative 0;	Mismatches 5;	Indels 8;	Gaps 1;
Qy	2	VQLVQSGAEVKKPGESLKISKCKSGSYFTSYWIGVWRQMPGKGLWMMGIIYPGSDSTRYS	61	
Db	2	VQLVQSGAEVKKPGESLKISKCKSGSYFTSYWIGVWRQMPGKGLWMMGIIYPGSDSTRYS	61	
Qy	62	PSFGQATISADKSIISTAYLQWSSLKASDAMYYCARHVDVGATIGSGYYYYYHGMVDWVGQ	121	
Db	62	PSFGQVIISADKSIISTAYLQWSSLKASDAMYYCAR-----TGDIYSYHGMDVDWVGQ	113	
Qy	122	GTTVTVSS	129	
Db	114	GTTVTVSS	121	

## RESULT 11

```

US-11-440-728-118
; Sequence 118, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; THEREOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-118

```

RESULT 12

```

US-11-440-728-90
; Sequence 90, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadai
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; THEREOF

```

```
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-90

Query Match      85.7%; Score 599; DB 7; Length 121;
Best Local Similarity 88.4%; Pred. No. 2.1e-48;
Matches 114; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIIPGDS DTRY 60
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIIPGDS DTRY 60
QY 61 SPSPGQQTISADKSI STAYLQWSSLKASDTAMYICARHVDVGCATIGGYYYHGM DVMWG 120
Db 61 SPSPGQQTISADKSI RTAYLQWSSLKASDTAMYICARHVDVGCATIGGYYYHGM DVMWG 112
QY 121 QGTTVTVSS 129
Db 113 QGTTVTVSS 121

RESULT 13
US-11-109-181-313
; Sequence 313, Application US/11/109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-313

Query Match      85.6%; Score 598.5; DB 7; Length 126;
Best Local Similarity 86.5%; Pred. No. 2.5e-48;
Matches 115; Conservative 1; Mismatches 6; Indels 11; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIIPGDS DTRY 60
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIIPGDS DTRY 60
QY 61 SPSPGQQTISADKSI STAYLQWSSLKASDTAMYICARHVDVGCATIGGYYYHGM 116
Db 61 SPSPGQQTISADKSI STAYLQWSSLKASDTAMYICARHVDVGCATIGGYYYHGM 113
QY 117 DWGQGTIVTVSS 129
Db 114 DWGQGTIVTVSS 126
```

```
RESULT 14
US-11-440-728-146
; Sequence 146, Application US/11/440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-146

Query Match      85.6%; Score 598; DB 7; Length 119;
Best Local Similarity 89.9%; Pred. No. 2.6e-48;
Matches 116; Conservative 0; Mismatches 3; Indels 10; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIIPGDS DTRY 60
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIIPGDS DTRY 60
QY 61 SPSPGQQTISADKSI STAYLQWSSLKASDTAMYICARHVDVGCATIGGYYYHGM DVMWG 120
Db 61 SPSPGQQTISADKSI STAYLQWSSLKASDTAMYICARHVDVGCATIGGYYYHGM DVMWG 110
QY 121 QGTTVTVSS 129
Db 111 QGTTVTVSS 119

RESULT 15
US-11-440-728-98
; Sequence 98, Application US/11/440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-98

Query Match      85.6%; Score 598; DB 7; Length 121;
Best Local Similarity 87.6%; Pred. No. 2.6e-48;
Matches 113; Conservative 3; Mismatches 5; Indels 8; Gaps 1;
```



```
QY 1 EVQLVQSGAEVKKPESLKISKKGSGYSFTSYWIGWVRQMPGKGLEWNGIIPGSDTRY 60
Db 1 EVQLVQSGAEVKKPESLKISKKGSGYSFTSYWIGWVRQMPGKGLEWNGIIPGSDTRY 60
QY 61 SPSPGQATISADKSIISTAYLQWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVWG 120
Db 61 SPSPGQVTISADKSIINTAYLQWSSLKASDTAMYICARQ-----GGHYYSGMVWG 112
QY 121 QGTTVTVSS 129
Db 113 QGTTVTVSS 121
```

Search completed: April 25, 2007, 04:27:43  
Job time : 49.7415 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 98 Seconds  
(without alignments) 564.248 Million cell u

**Title:** US-10-665-383-40

Perfect score: 590

Sequence: 1 DIVMTQSP<sup>1</sup>LSLPVTPGEPAS<sup>1</sup>.....MQALQSLMCSFGQGTKLEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Minimum	DB seq	length:	0
Maximum	DB seq	length:	2000000000

Post-processing: Minimum Match 0%

POST-PROCESSING: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 200701:\*

- 1: `gensseqp1980s*`
- 2: `gensseqp1990s*`
- 3: `gensseqp2000s*`
- 4: `gensseqp2001s*`
- 5: `gensseqp2002s*`
- 6: `gensseqp2003as*`
- 7: `gensseqp2003bs*`
- 8: `gensseqp2004s*`
- 9: `gensseqp2005s*`
- 10: `gensseqp2006s*`
- 11: `gensseqp2007s*`

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	590	100.0	113	7	ADK18931	Adk18931	Anti-huma
2	590	100.0	113	7	ADK18797	Adk18797	Anti-huma
3	590	100.0	113	7	ADK18606	Adk18606	Anti-huma
4	590	100.0	113	8	ADL25430	Adl25430	Human mAb
5	576.5	97.7	114	7	ADK18998	Adk18998	Anti-huma
6	556	94.2	248	4	AAg65590	Ag65590	Anti-hEDR
7	555	94.1	113	3	AAy95221	Aay95221	Anti-plat
8	554.5	94.0	131	10	AEJ57801	Aej57801	Human an
9	554.5	94.0	146	10	AEJ57944	Aej57944	Human an
10	554	93.9	113	3	AAy95220	Aay95220	Anti-plat
11	554	93.9	113	8	ADI22126	Adi22126	Anti-plat
12	554	93.9	114	3	AAy95186	Aay95186	Anti-plat
13	554	93.9	131	3	AAy95226	Aay95226	Anti-plat
14	550	93.2	112	8	ADP47300	Adp47300	Human pho
15	550	93.2	223	10	AEK98277	Aek98277	Human 16
16	550	93.2	223	10	AEK98219	Aek98219	Human 16
17	549	93.1	113	8	ADI22125	Adi22125	Anti-plat
18	548.5	93.0	110	7	ADP03995	Adp03995	Murine-ex
19	548.5	93.0	112	8	ADI22111	Adi22111	Anti-plat
20	547.5	92.8	112	8	ADI22129	Adi22129	Anti-plat
21	547.5	92.8	112	8	ADI22112	Adi22112	Anti-plat
22	547	92.7	111	3	AAy95225	Aay95225	Anti-plat

## ALIGNMENTS

## RESULT 1

ADK18831

ID ADK18831 standard; protein; 113 AA.

ADK18831;

06-MAY-2004 (first entry)

DE Anti-human PDGF-D antibody protein related sequence #57.

antiinflammatory: immunomodulator: cytostatic: gene therapy.

XX Homo sapiens.

XX  
PN  
W02003057857-A2XX  
17-ПТ.-2003XX  
PF 06-TAN-2003. 2003WQ-IIS000398XX  
PB  
07-TAN-2002- 2002US-00041860XX  
PA (ABGE-) ARCENTY TNC

XX	Corvalan JPF	Jia Y	Feng Y	Chen F	Gazit G	Weber B.
PI						

PI Corvairan U  
PI Bezabeh B:

WPT: 2003-587119/55

PT New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

XX  
PS  
Disclosure: SEO ID NO 255. 255nn. English.

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D), were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

XX	SQ	Sequence 113 AA;
	Query Match	100.0%; Score 590; DB 7; Length 113;
	Best Local Similarity	100.0%; Pred. No. 3.1e-43;
	Matches 113; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	DIVMTQSPISLPVTPGEPASISCRSSQSLLHSGNYNDWYLQKPGQSPOLLIIYIGSNRA 60
DB	1	DIVMTQSPISLPVTPGEPASISCRSSQSLLHSGNYNDWYLQKPGQSPOLLIIYIGSNRA 60
QY	61	SGVPDRFSGSGGTDFTLKISRVEADGVGYVCMAQLSLMCSFGQGTKLEIK 113
DB	61	SGVPDRFSGSGGTDFTLKISRVEADGVGYVCMAQLSLMCSFGQGTKLEIK 113
 RESULT 2		
ID	ADK18797	
ID	ADK18797 standard; protein; 113 AA.	
XX	AC	ADK18797;
XX	AC	ADK18797;
DT	06-MAY-2004	(first entry)
XX	XX	
DE	Anti-human PDGF-D antibody protein related sequence #23.	
XX	XX	
KW	antiinflammatory; immunomodulator; cytostatic; gene therapy.	
OS	Homo sapiens.	
XX	XX	
PN	W02003057857-A2.	
XX	XX	
PD	17-JUL-2003.	
XX	XX	
PJ	06-JAN-2003; 2003WO-US000398.	
PF	XX	
XX	XX	
PR	07-JAN-2002; 2002US-00041860.	
XX	XX	
PA	(ABGE-) ABGENIX INC.	
XX	XX	
PI	Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;	
PI	Bezabeh B;	
XX	XX	
DR	WPI; 2003-587119/55.	
XX	XX	
PT	New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.	
PT	Disclosure; SEQ ID NO 221; 255pp; English.	
XX	XX	
CC	The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HBK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.	
CC	clone 30664188.0.99 arising in the conditioned medium obtained when HBK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.	
XX	XX	
SQ	Sequence 113 AA;	
	Query Match	100.0%; Score 590; DB 7; Length 113;
	Best Local Similarity	100.0%; Pred. No. 3.1e-43;
	Matches 113; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	DIVMTQSPISLPVTPGEPASISCRSSQSLLHSGNYNDWYLQKPGQSPOLLIIYIGSNRA 60
DB	1	DIVMTQSPISLPVTPGEPASISCRSSQSLLHSGNYNDWYLQKPGQSPOLLIIYIGSNRA 60
QY	.61	SGVPDRFSGSGGTDFTLKISRVEADGVGYVCMAQLSLMCSFGQGTKLEIK 113

DE Human mAb 1.29 light chain variable region protein SEQ ID NO:40.  
XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;  
KW nephritis; mesangial cell proliferation inhibition;  
KW mesangial proliferative glomerulonephritis; nephrotropic;  
KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;  
KW gene therapy; human; monoclonal antibody; mAb.  
XX  
XX Homo sapiens.  
XX WO2004024098-A2.  
PN  
XX 25-MAR-2004.  
PD  
XX 16-SEP-2003; 2003WO-US029414.  
PF  
XX 16-SEP-2002; 2002US-0411137P.  
PR  
XX (ABGE-) ABGENIX INC.  
PA (CURA-) CURAGEN CORP.  
PI Floege J, Garit-Bornstein G, Keyt B, Larochelle WJ, Lichenstein H;  
XX WPI; 2004-269881/25.  
DR N-PSDB; ADL25429.  
DR  
XX Use of an antibody or its binding fragment that binds platelet derived  
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating  
PT nephritis.  
PT  
XX Disclosure; SEQ ID NO 40; 115pp; English.  
PS  
XX The present invention describes an antibody or its binding fragment that  
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is  
CC useful in preparing a medicament for treating nephritis. Also described:  
CC (1) a method of detecting nephritis; (2) a method of treating nephritis;  
CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method  
CC of treating mesangial proliferative glomerulonephritis. The antibody has  
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and  
CC antidiabetic activities, and can be used in gene therapy. The antibody or  
CC its binding fragment, that binds PDGF-DD, can be used in preparing a  
CC medicament for treating nephritis and related disorders, e.g., mesangial  
CC proliferative glomerulonephritis. The present sequence represents a human  
CC monoclonal antibody (mAb) variable region sequence, which is used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 113 AA;  
Query Match 100.0%; Score 590; DB 8; Length 113;  
Best Local Similarity 100.0%; Pred. No. 3.1e-43; Mismatches 0; Indels 0; Gaps 0;  
Matches 113; Conservative 0;  
QY 1 DIVMTQSLPLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSQPLLIIYLSNRA 60  
DB 1 DIVMTQSLPLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSQPLLIIYLSNRA 60  
QY 61 SGVPRFSGSGSGTDTFTLKISRVEADDDGVYVYCMQALQSLMCSFGQGTKEIK 113  
DB 61 SGVPRFSGSGSGTDTFTLKISRVEADDDGVYVYCMQALQSLMCSFGQGTKEIK 113  
RESULT 5  
ADK18898  
ID ADK18898 standard; protein; 114 AA.  
XX  
XX ADK18898;  
XX  
XX 06-MAY-2004 (first entry)  
DT  
XX Anti-human PDGF-D antibody protein related sequence #124.  
DE  
XX  
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
XX

OS Homo sapiens.  
XX WO2003057857-A2.  
PN  
XX 17-JUL-2003.  
PD  
XX 06-JAN-2003; 2003WO-US000398.  
PF  
XX 07-JAN-2002; 2002US-00041860.  
PR  
XX (ABGE-) ABGENIX INC.  
PA  
XX Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX WPI; 2003-587119/55.  
DR  
XX New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
PT  
XX Disclosure; SEQ ID NO 322; 255pp; English.  
PS  
XX The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX  
XX Sequence 114 AA;  
Query Match 97.7%; Score 576.5; DB 7; Length 114;  
Best Local Similarity 98.2%; Pred. No. 4.6e-42;  
Matches 112; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
QY 1 DIVMTQSLPLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSQPLLIIYLSNRA 60  
DB 1 DIVMTQSLPLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSQPLLIIYLSNRA 60  
QY 61 SGVPRFSGSGSGTDTFTLKISRVEADDDGVYVYCMQALQSLMCSFGQGTKEIK 113  
DB 61 SGVPRFSGSGSGTDTFTLKISRVEADDDGVYVYCMQALQSLMCSFGQGTKEIK 114  
RESULT 6  
AAG65590  
ID AAG65590 standard; protein; 248 AA.  
XX  
XX AAG65590;  
XX  
XX 07-JAN-2002 (first entry)  
DT  
XX Anti-hEDRF antibody e9 amino acid sequence.  
DE  
XX Human; erythroid differentiation related factor; hEDRF; antianemic;  
KW erythrocyte deficiency; antibody e9.  
KW  
XX Homo sapiens.  
OS  
XX EP1130030-A1.  
PN  
XX 05-SEP-2001.  
PD  
XX 27-FEB-2001; 2001EP-00104821.  
PF  
XX 02-MAR-2000; 2000US-00517225.  
PR  
XX (HOFF ) ROCHE DIAGNOSTICS CORP.  
PA

XX Xu H, Mahoney W, Schueler P, Harriman WD;  
 PI WPI; 2001-608195/70.  
 DR N-PSDB; AAH47762.  
 XX Novel human erythroid differentiation related factor and polynucleotides  
 PT encoding it useful for treating anemia and other erythrocyte deficiencies  
 PT and for detecting expression of the factor in humans.  
 XX Disclosure; Fig 4; 29pp; English.  
 XX The invention provides a human erythroid differentiation related factor  
 CC (hEDRF). The hEDRF polypeptide and the encoding polynucleotide are useful  
 CC for treating anemias and other erythrocyte deficiencies. The hEDRF  
 CC protein is useful for producing antibodies, useful in screening assays to  
 CC identify pharmaceutical compounds of interest and compounds which bind to  
 CC hEDRF. The polynucleotides are useful for producing hEDRF or its related  
 CC polypeptides. The antibodies are useful for separating or detecting the  
 CC corresponding antigen e.g. for detection/quantitation of hEDRF in samples  
 CC taken from human subjects. Quantification of hEDRF at immunohistochemical  
 CC level finds value in evaluating the potential of the tissue site to  
 CC contribute towards the production of new erythroid cells. The present  
 CC sequence represents the amino acid sequence of an anti-hEDRF antibody e9  
 XX Sequence 248 AA;  
 SQ  
 Query Match 94.2%; Score 556; DB 4; Length 248;  
 Best Local Similarity 93.8%; Pred. No. 6.1e-40;  
 Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60  
 DB 135 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 194  
 QY 61 SGVPRFSGSGGTDFTLKISRVEADGVVYCMQALQSLMCSFGQGTGLEIK 113  
 DB 195 SGVPRFSGSGGTDFTLKISRVEADGVVYCMQALQSLMCSFGQGTGLEIK 247  
 RESULT 7  
 AAAY95221  
 ID AAAY95221 standard; protein; 113 AA.  
 AC AAAY95221;  
 DT 29-AUG-2000 (first entry)  
 XX Anti-platelet glycoprotein Ib human HIB-5 VL.  
 XX Variable light chain; single chain antibody; scFv; human; HIB-5;  
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
 KW antithrombotic; thrombus; therapy; diagnostic.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FT Region 1..23  
 FT /note= "framework region 1"  
 FT Region 24..39  
 FT /note= "complementarity determining region 1"  
 FT Region 40..54  
 FT /note= "framework region 2"  
 FT Region 55..61  
 FT /note= "complementarity determining region 2"  
 FT Region 62..93  
 FT /note= "framework region 3"  
 FT Region 94..101  
 FT /note= "complementarity determining region 3"  
 FT Region 102..113  
 FT /note= "framework region 4"  
 XX WO200026667-A1.

XX 11-MAY-2000.  
 PD 29-OCT-1999; 99WO-US025495.  
 XX 30-OCT-1998; 98US-0106275P.  
 PR (MILL/) MILLER J L.  
 PA Miller JL;  
 PI WPI; 2000-365744/31.  
 DR Isolated nucleic acid molecule encoding anti-human platelet glycoprotein  
 XX Ib alpha molecule useful for producing antibodies which inhibit platelet  
 PT aggregation.  
 PT Claim 18; Fig 8; 89pp; English.  
 PS The present sequence is that of the light chain variable region (VL) of  
 CC human single chain antibody (scFv) HIB-5, which is directed against  
 CC platelet glycoprotein Ib (GPIb). The HIB series of scFv was isolated from  
 CC a human synthetic VH and VL scFv library by 3 rounds of phagemid  
 CC selection against transfected CHO cells expressing the GPIb alpha  
 CC component of the GPIb/IX/V complex on their surface, followed by a 4th  
 CC round of selection against washed human platelets, and 2 final rounds in  
 CC which attempts were made to displace scFv from washed platelets by  
 CC flooding with murine monoclonal antibody or mimotope peptide (see  
 CC AAAY95229). Whether displayed as surface proteins on a phagemid or  
 CC secreted as free scFv by Escherichia coli, the HIB scFv clones are  
 CC capable of inhibiting von Willebrand factor-dependent aggregation of  
 CC platelets. The scFv are composed of native human protein sequences and  
 CC are therefore attractive potential reagents for therapeutic purposes.  
 CC They provide a new class of antithrombotic agents, useful for the  
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass  
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.  
 CC Methods of inhibiting aggregation of platelets, of binding human platelet  
 CC GPIb alpha and of selecting a VH or VL region of an antibody that  
 CC inhibits platelet aggregation are claimed. Note: The present sequence is  
 CC not shown in the specification but is derived from the HIB-5 VH sequence  
 CC given in Fig 8 (see AAAY95220)  
 XX Sequence 113 AA;  
 SQ  
 Query Match 94.1%; Score 555; DB 3; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 3.2e-40;  
 Matches 107; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60  
 DB 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60  
 QY 61 SGVPRFSGSGGTDFTLKISRVEADGVVYCMQALQSLMCSFGQGTGLEIK 113  
 DB 61 SGVPRFSGSGGTDFTLKISRVEADGVVYCMQALQSLMCSFGQGTGLEIK 113  
 RESULT 8  
 AEJ57801  
 ID AEJ57801 standard; protein; 131 AA.  
 XX AEJ57801;  
 AC AEJ57801;  
 DT 05-OCT-2006 (first entry)  
 XX Human antibody enzyme V-kappa2 VL PHVK-1 #1, SEQ.4.  
 DE Abzyme; antibody; immunoglobulin; infection; antimicrobial; cancer;  
 KW cytostatic; diagnostic; peptidase; light chain variable region; enzyme.  
 OS Homo sapiens.  
 XX JP2006197930-A.

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XX 03-AUG-2006.
XX 22-DEC-2005; 2005JP-00370880.
XX 22-DEC-2004; 2004JP-00372206.
XX (HIRO-) HIROSHIMA KEN.
XX Uda T, Hifumi M;
XX WPI; 2006-544634/56.
XX N-PSDB; AEJ57943.
XX New human enzyme antibody consisting of light chain or heavy chain
XX polypeptides encoded by human germ line gene e.g. L22 and VH1-24, useful
XX for treatment and diagnosis of infectious diseases and cancer.
XX Claim 5; SEQ ID NO 4; 30pp; Japanese.
XX The invention relates to a human antibody enzyme (abzyme) having high
XX recognition ability and high enzyme activity. The antibody enzyme
XX comprises a light chain encoded by a human germ line gene selected from
XX L22, V1-9, V1-13, V1-18, V1-22, V2-6, V2-7, V2-8, V2-13, V2-14, V3-3, A1,
XX A2, A3, A5, A7, A10, A17, A18, A19, A23, A26, A30, L14 and L22, and a
XX heavy chain encoded by a human germ line gene selected from VH1-24, VH3-
XX 9, VH3-13, VH3-16, VH3-20, VH3-30, VH3-33, VH3-35, VH3-43, VH3-64, VH3-
XX 72, VH3-73, VH3-74, VH4-34 and VH7-81. The invention also relates to a
XX method for producing a human antibody enzyme belonging to a particular
XX subgroup involving selection of human lymphocyte cDNAs encoding an
XX antibody with enzymatic activity using a primer based on a subgroup-
XX specific sequence. The antibody enzymes of the invention can be used in a
XX variety of fields, such as the medical industry, pharmaceutical industry,
XX reagent industry, medical equipment industry or food industry. The
XX antibody enzymes are useful in the diagnosis and treatment of medical
XX conditions such as cancer and various infectious diseases, and can also
XX be used in biosensors and biomaterials. The antibody enzymes exhibit high
XX in vivo efficacy for therapeutic applications, and can be produced
XX efficiently. The present sequence represents a specifically claimed V-
XX kappa2 light chain variable region (VL) of a human antibody enzyme having
XX peptidase activity. This sequence comprises a Ser-His-Asp (S-H-D)
XX catalytic triad. Note: The present sequence is shown in the sequence
XX listing of the specification and differs from the sequence also referred
XX to as VL pHVK-1 (AEJ57944) which is shown in Figure 18.
XX Sequence 131 AA;
XX Query Match 94.0%; Score 554.5; DB 10; Length 131;
XX Best Local Similarity 95.6%; Pred. No. 4.2e-40;
XX Matches 108; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
OY 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLIYLGSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLIYLGSNRA 60
OY 61 SGVPDRFSGSGGTDFTLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPDRFSGSGGTDFTLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 112
RESULT 9
AEJ57944
ID AEJ57944 standard; protein; 146 AA.
XX AC AEJ57944;
XX 05-OCT-2006 (first entry)
XX Human antibody enzyme V-kappa2 VL pHVK-1 #2.
XX Abzyme; antibody; immunoglobulin; infection; antimicrobial; cancer;
XX cytostatic; diagnostic; peptidase; light chain variable region; enzyme.
XX

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OS Homo sapiens.
XX JF2006197930-A.
XX 03-AUG-2006.
XX 22-DEC-2005; 2005JP-00370880.
XX 22-DEC-2004; 2004JP-00372206.
XX (HIRO-) HIROSHIMA KEN.
XX Uda T, Hifumi M;
XX WPI; 2006-544634/56.
XX N-PSDB; AEJ57943.
XX New human enzyme antibody consisting of light chain or heavy chain
XX polypeptides encoded by human germ line gene e.g. L22 and VH1-24, useful
XX for treatment and diagnosis of infectious diseases and cancer.
XX Example 3; Fig 18; 30pp; Japanese.
XX The invention relates to a human antibody enzyme (abzyme) having high
XX recognition ability and high enzyme activity. The antibody enzyme
XX comprises a light chain encoded by a human germ line gene selected from
XX L22, V1-9, V1-13, V1-18, V1-22, V2-6, V2-7, V2-8, V2-13, V2-14, V3-3, A1,
XX A2, A3, A5, A7, A10, A17, A18, A19, A23, A26, A30, L14 and L22, and a
XX heavy chain encoded by a human germ line gene selected from VH1-24, VH3-
XX 9, VH3-13, VH3-16, VH3-20, VH3-30, VH3-33, VH3-35, VH3-43, VH3-64, VH3-
XX 72, VH3-73, VH3-74, VH4-34 and VH7-81. The invention also relates to a
XX method for producing a human antibody enzyme belonging to a particular
XX subgroup involving selection of human lymphocyte cDNAs encoding an
XX antibody with enzymatic activity using a primer based on a subgroup-
XX specific sequence. The antibody enzymes of the invention can be used in a
XX variety of fields, such as the medical industry, pharmaceutical industry,
XX reagent industry, medical equipment industry or food industry. The
XX antibody enzymes are useful in the diagnosis and treatment of medical
XX conditions such as cancer and various infectious diseases, and can also
XX be used in biosensors and biomaterials. The antibody enzymes exhibit high
XX in vivo efficacy for therapeutic applications, and can be produced
XX efficiently. The present sequence represents a V-kappa2 light chain
XX variable region (VL) of a human antibody enzyme having peptidase
XX activity. This sequence comprises a Ser-His-Asp (S-H-D) catalytic triad.
XX Note: The present sequence is shown in Figure 18 of the specification and
XX differs from the sequence also referred to as VL pHVK-1 (AEJ57801) which
XX is shown in the sequence listing.
XX Sequence 146 AA;
XX Query Match 94.0%; Score 554.5; DB 10; Length 146;
XX Best Local Similarity 95.6%; Pred. No. 4.7e-40;
XX Matches 108; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
OY 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLIYLGSNRA 60
Db 16 DIVMTQSLPLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLIYLGSNRA 75
OY 61 SGVPDRFSGSGGTDFTLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 113
Db 76 SGVPDRFSGSGGTDFTLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 127
RESULT 10
AAJ95220
ID AAJ95220 standard; protein; 113 AA.
XX AC AAJ95220;
XX 29-AUG-2000 (first entry)
XX Anti-platelet glycoprotein Ib human H1b-5 VL.
XX

```

Variable light chain; single chain antibody; scFv; human; H1b-5;  
glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
antithrombotic; thrombus; therapy; diagnostic.

Homo sapiens.

# Location/Qualifiers

Key  
Region 1. .23  
/note= "framework region 1"  
Region 24. .39  
/note= "complementarity determining region 1"  
Region 40. .54  
/note= "framework region 2"  
Region 55. .61  
/note= "complementarity determining region 2"  
Region 62. .93  
/note= "framework region 3"  
Region 94. .101  
/note= "complementarity determining region 3"  
Region 102. .113  
/note= "framework region 4"

WO200026667-A1.

11-MAY-2000.

29-OCT-1999; 99WO-US025495.

30-OCT-1998; 98US-0106275P.

(MILLER) MILLER J L.

Miller JL;

WPI; 2000-365744/31.

Isolated nucleic acid molecule encoding anti-human platelet glycoprotein  
Ib alpha molecule useful for producing antibodies which inhibit platelet  
aggregation.

Claim 18; Fig 8; 89pp; English.

The present sequence is that of the light chain variable region (VL) of  
human single chain antibody (scFv) H1b-5, which is directed against  
platelet glycoprotein Ib (GP1b). The H1b series of scFv was isolated from  
a human synthetic VH and VL scFv library by 3 rounds of phagemid  
selection against transfected CHO cells expressing the GP1b alpha  
component of the GP1b/IX/V complex on their surface, followed by a 4th  
round of selection against washed human platelets, and 2 final rounds in  
which attempts were made to displace scFv from washed platelets by  
flooding with murine monoclonal antibody or mimotope peptide (see  
AA95229). Whether displayed as surface proteins on a phagemid or  
secreted as free scFv by *Escherichia coli*, the H1b scFv clones are  
capable of inhibiting von Willebrand factor-dependent aggregation of  
platelets. The scFv are composed of native human protein sequences and  
are therefore attractive potential reagents for therapeutic purposes.  
They provide a new class of antithrombotic agents, useful for the  
prevention of platelet-dependent thrombi in diseased arteries, bypass  
grafts, dialysis etc., and can also be used as diagnostic reagents.  
Methods of inhibiting aggregation of platelets, of binding human platelet  
GP1b alpha and of selecting a VH or VL region of an antibody that  
inhibits platelet aggregation are claimed

Sequence 113 AA;

Query Match 93.9%; Score 554; DB 3; Length 113;

Best Local Similarity 93.8%; Pred. No. 4e-40;  
Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

1 DIVMTQSLPLSVPTGEPASISCRSSQSLHNGVNYLDWYLOKPGQSPQLLYLGSNRA 60

1 DIVMTQSLPLSVPTGEPASISCRSSQSLHNGVNYLDWYLOKPGQSPQLLYLGSNRA 60

QY

Db

RESULT 11

ADI22126

XX ADI22126 standard; protein; 113 AA.

XX ADI22126;

XX 22-APR-2004 (first entry)

XX Anti-platelet autoantibody related light chain amino acid L50 SEQ:89.

XX anti-platelet autoantibody; autoantibody; blood clotting inhibition;  
thrombus; platelet adhesion inhibition;  
thrombotic thrombocytopenic purpura; platelet aggregation inhibition;  
idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;  
thrombolytic; human.

XX Homo sapiens.

XX Synthetic.

XX WO2004005890-A2.

XX 15-JAN-2004.

XX 03-JUL-2003; 2003WO-US021304.

XX 03-JUL-2002; 2002US-0394352P.

XX 18-SEP-2002; 2002US-0411694P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI; 2004-142998/14.

XX N-PSDB; ADI22073.

XX Claim 12; SEQ ID NO 89; 232pp; English.

The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein Iib/Iiia, where the autoantibody, or its fragment comprises an antigen binding region derived from an H4L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein Iib/Iiia, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing

CC and for developing therapeutics for diseases mediated by autoantibody  
 CC binding with platelet antigens.. (M6) and (M12) are useful for treating  
 CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic  
 CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood  
 CC clotting. The present sequence is used in the exemplification of the  
 CC present invention.

XX SQ Sequence 113 AA;  
 Query Match 93.9%; Score 554; DB 8; Length 113;  
 Best Local Similarity 93.8%; Pred. No. 4e-40; Indels 0; Gaps 0;  
 Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSPILSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLYQKPGQSPQLLIYLGSNRA 60

DB 1 DIVMTQSPILSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLYQKPGQSPQLLIYLGSNRA 60

QY 61 SGVDPFRFSGSGGTDTFLKISRVEADVGVYCMQALQSLMCSFGQGTLEIK 113

DB 61 SGVDPFRFSGSGGTDTFLKISRVEADVGVYCMQALQTRPVTFGQGTLEIK 113

#### RESULT 12

AA95186  
 ID AAY95186 standard; protein; 114 AA.

XX AC AAY95186;

DT 29-AUG-2000 (first entry)

XX Anti-platelet glycoprotein Ib human H1b-5 VL.

DE Variable light chain; single chain antibody; scFv; human; H1b-5;

KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;

KW antithrombotic; thrombus; therapy; diagnostic.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..23

FT /note= "framework region 1"

FT Region 24..39

FT /note= "complementarity determining region 1"

FT Region 40..54

FT /note= "framework region 2"

FT Region 55..61

FT /note= "complementarity determining region 2"

FT Region 62..93

FT /note= "framework region 3"

FT Region 94..101

FT /note= "complementarity determining region 3"

FT Region 102..114

FT /note= "framework region 4"

XX WO200026667-A1.

XX PD 11-MAY-2000.

XX PF 29-OCT-1999; 99WO-US025495.

XX PR 30-OCT-1998; 98US-0106275P.

XX PA (MILL/) MILLER J L.

XX PI Miller JL;

XX DR WPI: 2000-365744/31.

XX DR N-PSDB; AAA27664.

XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein

PT Ib alpha molecule useful for producing antibodies which inhibit platelet

PT aggregation.

XX

PS Claim 11; Page 77; 89pp; English.

XX The present sequence is that of the light chain variable region (VL) of  
 CC human single chain antibody (scFv) H1b-5, which is directed against  
 CC platelet glycoprotein Ib (GP1b). The H1b scFv was isolated from  
 CC a human synthetic VH and VL scFv library by 3 rounds of phagemid  
 CC selection against transfected CHO cells expressing the GP1b alpha  
 CC component of the GP1b/IX/V complex on their surface, followed by a 4th  
 CC round of selection against washed human platelets, and 2 final rounds in  
 CC which attempts were made to displace scFv from washed platelets by  
 CC flooding with murine monoclonal antibody or mimotope peptide (see  
 CC AAY95229). Whether displayed as surface proteins on a phagemid or  
 CC secreted as free scFv by *Escherichia coli*, the H1b scFv clones are  
 CC capable of inhibiting von Willebrand factor-dependent aggregation of  
 CC platelets. The scFv are composed of native human protein sequences and  
 CC are therefore attractive potential reagents for therapeutic purposes.  
 CC They provide a new class of antithrombotic agents, useful for the  
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass  
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.  
 CC Methods of inhibiting aggregation of platelets, of binding human platelet  
 CC GP1b alpha and of selecting a VH or VL region of an antibody that  
 CC inhibits platelet aggregation are claimed

XX SQ Sequence 114 AA;

Query Match 93.9%; Score 554; DB 3; Length 114;

Best Local Similarity 93.8%; Pred. No. 4e-40; Indels 0; Gaps 0;  
 Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSPILSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLYQKPGQSPQLLIYLGSNRA 60

DB 1 DIVMTQSPILSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLYQKPGQSPQLLIYLGSNRA 60

QY 61 SGVDPFRFSGSGGTDTFLKISRVEADVGVYCMQALQSLMCSFGQGTLEIK 113

DB 61 SGVDPFRFSGSGGTDTFLKISRVEADVGVYCMQALQTPFPFQGTLEIK 113

#### RESULT 13

AA95226

ID AAY95226 standard; protein; 131 AA.

XX AC AAY95226;

DT 29-AUG-2000 (first entry)

XX Anti-platelet glycoprotein Ib human H1b-5 VL region and linker.

DE Variable light chain; single chain antibody; scFv; human; H1b-5;

KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;

KW antithrombotic; thrombus; therapy; diagnostic.

XX OS Synthetic.

OS Homo sapiens.

XX Chimeric.

XX Key Location/Qualifiers

FT Peptide 1..17

FT /note= "vector-derived linker"

FT Region 18..131

FT /note= "light chain variable region"

FT Region 18..40

FT /note= "framework region 1"

FT Region 41..56

FT /note= "complementarity determining region 1"

FT Region 57..71

FT /note= "framework region 2"

FT Region 72..78

FT /note= "complementarity determining region 2"

FT Region 79..110

FT /note= "framework region 3"

FT Region 111..119

FT /note= "complementarity determining region 3"



FT Region 120. .131  
/note= "framework region 4"

FN WO200026667-A1.  
XX 11-MAY-2000.  
XX 29-OCT-1999; 99WO-US025495.  
XX 30-OCT-1998; 98US-0106275P.  
XX (MILLER) MILLER J L.  
XX Miller JL;  
XX WPI; 2000-365744/31.  
XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein  
PT Ib alpha molecule useful for producing antibodies which inhibit platelet  
PT aggregation.  
XX Disclosure; Fig 8; 89pp; English.  
XX The present sequence is that of the light chain variable region (VL) plus  
CC linker peptide of human single chain antibody (scFv) H1B-5, which is  
CC directed against platelet glycoprotein Ib (GP1b). H1B-5 is composed of a  
CC heavy chain variable region and light chain variable region joined via a  
CC vector-derived peptide linker. The H1B series of scFv was isolated from a  
CC human synthetic VH and VL scFv library by 3 rounds of phagemid selection  
CC against transfected CHO cells expressing the GP1b alpha component of the  
CC GP1b/IX/V complex on their surface, followed by a 4th round of selection  
CC against washed human platelets, and 2 final rounds in which attempts were  
CC made to displace scFv from washed platelets by flooding with murine  
CC monoclonal antibody or mimotope peptide (see AA95229). Whether displayed  
CC as surface proteins on a phagemid or secreted as free scFv by Escherichia  
CC coli, the H1B scFv clones are capable of inhibiting von Willebrand factor  
CC dependent aggregation of platelets. The scFv are composed of native  
CC human protein sequences and are therefore attractive potential reagents  
CC for therapeutic purposes. They provide a new class of antithrombotic  
CC agents, useful for the prevention of platelet-dependent thrombi in  
CC diseased arteries, bypass grafts, dialysis etc., and can also be used as  
CC diagnostic reagents. Methods of inhibiting aggregation of platelets, of  
CC binding human platelet GP1b alpha and of selecting a VH or VL region of  
CC an antibody that inhibits platelet aggregation are claimed  
XX  
SQ Sequence 131 AA;  
Query Match 93.9%; Score 554; DB 3; Length 131;  
Best Local Similarity 93.8%; Pred. No. 4.6e-40;  
Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHLSNGYNYLDWYQKPGQSPQLLIYLGSNRA 60  
Db 18 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHLSNGYNYLDWYQKPGQSPQLLIYLGSNRA 77  
QY 61 SGVPRFSGSGGTFTLKISRVEADGVVYCMQALQSLMCSFGQGTGLEIK 113  
Db 78 SGVPRFSGSGGTFTLKISRVEADGVVYCMQALQTPPTFGQGTGLEIK 130

RESULT 14  
ADP47300  
ID ADP47300 standard; protein; 112 AA.  
XX ADP47300;  
XX  
XX ADP47300;  
DT 09-SEP-2004 (first entry)  
DE Human phospholipase A2-specific monoclonal antibody light chain #20.  
XX human; monoclonal antibody; phospholipase A2; PLA2;  
KW inflammatory disorder; degenerative disorder;  
KW joint inflammatory reaction; skin inflammatory reaction;

KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;  
KW Alzheimer's disease; atherosclerosis; restenosis; light chain.  
OS Homo sapiens.  
XX WO2004050850-A2.  
XX 17-JUN-2004.  
XX 02-DEC-2003; 2003WO-US038234.  
XX 02-DEC-2002; 2002US-0430724P.  
XX (ABGE-) ABGENIX INC.  
XX (LEXI-) LEXICON GENETICS INC.  
XX Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;  
PI Jia X, Nocerini MR;  
XX WPI; 2004-461119/43.  
XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),  
PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,  
PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.  
XX Example 5; SEQ ID NO 215; 128pp; English.  
XX The invention comprises a human monoclonal antibody that binds to  
CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is  
CC useful in the preparation of a medicament for the treatment of  
CC inflammatory and degenerative disorders stemming from inflammatory  
CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,  
CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present  
CC amino acid sequence represents the light chain from a monoclonal antibody  
CC that is specific for the human phospholipase A2 (PLA2) enzyme.  
XX  
SQ Sequence 112 AA;  
Query Match 93.2%; Score 550; DB 8; Length 112;  
Best Local Similarity 93.8%; Pred. No. 8.7e-40;  
Matches 106; Conservative 5; Mismatches 0; Indels 2; Gaps 1;

QY 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHLSNGYNYLDWYQKPGQSPQLLIYLGSNRA 60  
Db 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHLSNGYNYLDWYQKPGQSPQLLIYLGSNRA 60  
QY 61 SGVPRFSGSGGTFTLKISRVEADGVVYCMQALQSLMCSFGQGTGLEIK 113  
Db 61 SGVPRFSGSGGTFTLKISRVEADGVVYCMQALQTI--TFGQGTGLEIK 111

RESULT 15  
AEK98277  
ID AEK98277 standard; protein; 223 AA.  
XX AEK98277;  
XX  
XX 30-NOV-2006 (first entry)  
XX Human 161P2F10B antibody light chain SEQ ID NO 156.  
DE  
XX Cytostatic; 161P2F10B antagonist; Gene therapy; antibody production;  
KW cancer; neoplasm; therapeutic; light chain.  
XX Homo sapiens.  
XX WO2006105488-A2.  
XX 05-OCT-2006.  
XX 31-MAR-2006; 2006WO-US012314.  
XX 31-MAR-2005; 2005US-0667588P.  
PR

PR 20-JUL-2005; 2005US-0700975P.  
XX PA (AGEN-) AGENSYS INC.  
XX  
XX Jakobovits A, Kanner SB, Challita-Eid PM, Perez-Villar JJ;  
PI Satpaev D, Raitano AB, Morrison RK, Morrison KJM, Jia X, Gudas J;  
XX WPI; 2006-680690/70.  
DR  
XX New monoclonal antibody that binds specifically to a 161P2F10B protein,  
PT useful for treating prostate, pancreas, bladder, kidney, colon, lung,  
PT ovary, or breast cancer.  
XX  
PS Disclosure; SEQ ID NO 156; 438pp; English.  
XX  
XX The invention relates to a monoclonal antibody or its antigen binding  
CC fragment comprising an antigen binding site that binds specifically to a  
CC 161P2F10B protein, where the monoclonal antibody is H16-7.213, H16-9.69,  
CC H16-1.52, H16-1(1)23, H16-9.44, H16-1.67, H16-1(3,5)36, H16-1.86, H16-  
CC 9.10, H16-9.33, H16-1(1)11, H16-1(3,5)18, H16-1(2,4)4, H16-  
CC -1(3,5)56, H16-1.93, H16-7.8, H16-1(3,5)27.1, H16-1.61, H16-1(3,5)5, H16-  
CC -7.200, H16-1(3,5)42, H16-9.65, H16-1.29, H16-3.4, H16-1.92, H16-  
CC 1(3,5)19, or H16-1.80. The monoclonal antibody or its fragment is useful  
CC for preparing a medicament for the treatment of prostate, pancreas,  
CC bladder, kidney, colon, lung, ovary, or breast cancer, where the  
CC monoclonal antibody or its fragment is administered in combination with  
CC radiation or a chemotherapeutic agent. The present sequence represents  
CC the amino acid sequence of a human 161P2F10B antibody light chain.  
XX  
SQ Sequence 223 AA;  
Query Match 93.2%; Score 550; DB 10; Length 223;  
Best Local Similarity 93.8%; Pred. No. 1.8e-39;  
Matches 106; Conservative 5; Mismatches 0; Indels 2; Gaps 1;  
OY 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRA 60  
DB 8 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRA 67  
OY 61 SGVPRFSGSGSGTDFTLKISRVEADDDVGYTCMQALQSLMCSFGQGTKEIK 113  
DB 68 SGVPRFSGSGSGTDFTLKISRVEADDDVGYTCMQALQTI--TFGQGTREIK 118

Search completed: April 25, 2007, 04:05:21  
Job time : 98.9972 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 9 Seconds  
(without alignments)  
1261.509 Million cell updates/sec

Title: US-10-665-383-40  
Perfect score: 590  
Sequence: 1 DIVMTQSLPLVPTGEPAS.....MQALQSLMCSFGQGTKLEIK 113  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	545.5	92.5	132	2 S26882	Ig kappa chain V r
2	544.5	92.3	112	2 S58207	Ig light chain V r
3	544.5	92.3	135	2 S40342	Ig kappa chain - h
4	544.5	92.3	136	2 S40357	Ig kappa chain V-J
5	536.5	90.9	112	2 S58206	Ig light chain V r
6	535	90.7	126	2 S40339	Ig kappa chain - h
7	533.5	90.4	117	1 K2HUGM	Ig kappa chain pre
8	532.5	90.3	125	2 S40356	Ig kappa chain - h
9	508.5	86.2	113	1 K2HUTW	Ig kappa chain V-I
10	508.5	86.2	121	2 S40371	Ig kappa chain - h
11	508.5	86.2	131	2 S40372	Ig kappa chain V-J
12	505	85.6	123	2 S40319	Ig kappa chain V r
13	497	84.2	100	2 S24681	Ig kappa chain - h
14	487	82.5	114	2 S40375	Ig kappa chain - h
15	483.5	81.9	124	2 S03876	Ig kappa chain V-I
16	481	81.5	112	1 K2HUML	Ig kappa chain V-I
17	460	78.0	130	2 S40321	Ig kappa chain - h
18	456	77.3	115	1 K2HUCM	Ig kappa chain V-I
19	450.5	76.4	113	1 K2HUFU	Ig kappa chain V-I
20	447	75.8	87	2 S34091	Ig kappa chain V r
21	445	75.4	140	2 S22658	Ig kappa chain pre
22	442.5	75.0	112	2 F27887	Ig kappa chain V r
23	439.5	74.5	112	2 B27887	Ig kappa chain V r
24	439.5	74.5	113	2 PL0203	Ig kappa chain V r
25	439.5	74.5	126	2 S40312	anti-DNA autoantib
26	439.5	74.5	131	2 B39276	Ig kappa chain - h
27	439.5	74.5	131	2 D29380	Ig light chain pre
28	439	74.4	114	2 S49572	Ig kappa chain pre
29	439	74.4	130	2 C29380	Ig kappa chain pre

30	438	74.2	114	2 S40340	Ig kappa chain V-J
31	438	74.2	127	2 S40323	Ig kappa chain - h
32	437.5	74.2	115	2 S38715	Ig kappa chain V r
33	437.5	74.2	219	2 S52028	Ig kappa chain - m
34	436.5	74.0	131	2 B30577	Ig kappa chain pre
35	436.5	74.0	133	1 K2HURP	Ig kappa chain pre
36	436.5	74.0	142	2 S22902	Ig kappa chain V r
37	435.5	73.8	112	2 E27887	Ig kappa chain V r
38	435.5	73.8	112	2 S38719	Ig light chain V r
39	435.5	73.8	113	2 B41940	Ig light chain V r
40	435.5	73.8	118	2 PT0359	Ig kappa chain V r
41	435.5	73.8	131	2 B34904	Ig kappa chain pre
42	434.5	73.6	112	2 S53750	antibody Fab Jel 1
43	434.5	73.6	131	2 B32513	Ig kappa chain pre
44	433.5	73.5	96	2 S40320	Ig kappa chain - h
45	433.5	73.5	112	2 A31807	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S26882  
Ig kappa chain V region (V607) - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
C;Accession: S26882  
R;Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H.G.  
Nature 347, 90-92, 1990  
A;Title: Megabase inversions in the human genome as physiological events.  
A;Reference number: S26882; MUID:90370099; PMID:2118596  
A;Accession: S26882  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-132 <WEI>  
A;Cross-references: UNIPARC:UPI0000116D46; EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:16-95/Domain: immunoglobulin homology <IMM>  
A;Introns: 17/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match	92.5%	Score	545.5	DB	2	Length	132
Best Local Similarity	93.8%	Pred. No.	1.2e-42				
Matches	106	Conservative	4	Mismatches	2	Indels	1
Gaps	1						
QY	1	DIVMTQSLPLVPTGEPASISCRSSQSLHSGNYLDWYIQKPGQSPQLLIYLGSNRA	60				
DB	21	DIVMTQSLPLVPTGEPASISCRSSQSLHSGNYLDWYIQKPGQSPQLLIYLGSNRA	80				
QY	61	SGVPDRPSGSGGTDFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKLEIK	113				
DB	81	SGVPDRPSGSGGTDFTLKISRVEADVGYYVCMQALQTPQ-TFGQGTKVEIK	132				

RESULT 2

S58207  
Ig light chain V region anti-F(ab')2 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1996 #sequence\_revision 19-Apr-1996 #text\_change 21-Jan-2000  
C;Accession: S58207  
R;Welschof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, submitted to the EMBL Data Library, July 1995  
A;Description: Characterization of heavy and light chain immunoglobulin variable region  
A;Reference number: S58206  
A;Accession: S58207  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <WEL>  
A;Cross-references: UNIPARC:UPI0000116253; EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PI:16-95/Domain: immunoglobulin homology <IMM>

Query Match 92.3%; Score 544.5; DB 2; Length 112;  
Best Local Similarity 93.8%; Pred. No. 1.3e-42;  
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60  
DB 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60  
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVYCMQALQSLMCSFGQGTKEIK 113  
DB 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVYCMQALQSLMCSFGQGTKEIK 112

RESULT 3  
S40342  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 31-Dec-2004  
C:Accession: S40342  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40342  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-135 <KLE>  
A:Cross-references: UNIPROT:Q8NEK0; UNIPARC:UPI0000176CA7; EMBL:X72452; NID:G441372; PID:19-108/Domain: immunoglobulin homology <IMM>  
C:Superfamily: immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 92.3%; Score 544.5; DB 2; Length 135;  
Best Local Similarity 93.8%; Pred. No. 1.5e-42;  
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60  
DB 14 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 73  
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVYCMQALQSLMCSFGQGTKEIK 113  
DB 74 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVYCMQALQTPR-TFGQGTKEIK 125

RESULT 4  
S40357  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 31-Dec-2004  
C:Accession: S40357  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40357  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-136 <KLE>  
A:Cross-references: UNIPROT:Q8NEK0; UNIPARC:UPI0000176CA8; EMBL:X72467  
C:Superfamily: immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 92.3%; Score 544.5; DB 2; Length 136;  
Best Local Similarity 93.8%; Pred. No. 1.5e-42;  
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60  
DB 21 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 80

QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVYCMQALQSLMCSFGQGTKEIK 113  
DB 81 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVYCMQALQSLMCSFGQGTKEIK 132

RESULT 5  
S58206  
Ig light chain V region anti-F(ab')2 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jan-2000  
C:Accession: S58206  
R:Welshof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, R.;  
submitted to the EMBL Data Library, July 1995  
A:Description: Characterization of heavy and light chain immunoglobulin variable region  
A:Reference number: S58206  
A:Accession: S58206  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEL>  
A:Cross-references: UNIPARC:UPI0000116252; EMBL:X89054; NID:G929640; PIDN:CAA61441.1; PID:16-95/Domain: immunoglobulin homology <IMM>  
C:Superfamily: immunoglobulin  
C:Keywords: immunoglobulin

Query Match 90.9%; Score 536.5; DB 2; Length 112;  
Best Local Similarity 92.0%; Pred. No. 6.7e-42;  
Matches 104; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60  
DB 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYFDWYLQKPGQSPQLLIYLGSNRA 60  
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVYCMQALQSLMCSFGQGTKEIK 113  
DB 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVYCMQALQTPR-TFGGQGTKEIK 112

RESULT 6  
S40339  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40339  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40339  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-126 <KLE>  
A:Cross-references: UNIPARC:UPI0000116159; EMBL:X72449; NID:G441366; PIDN:CAA51117.1; PID:06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 90.7%; Score 535; DB 2; Length 126;  
Best Local Similarity 92.0%; Pred. No. 1e-41;  
Matches 104; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60  
DB 16 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 75  
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVYCMQALQSLMCSFGQGTKEIK 113  
DB 76 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVYCMQALQTP--WTFGQGTKEIK 126

RESULT 7  
K2HUGM  
Ig kappa chain precursor V-II region (GM607) - human (fragment)  
C:Species: Homo sapiens (man)

C>Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
C/Accession: A01889; B2452  
R/Klobeck, H.G.; Solomon, A.; Zachau, H.G.  
Nature 309, 73-76, 1984  
A/Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.  
A/Reference number: A01889; MUID:84191506; PMID:6325927  
A/Accession: A01889  
A/Molecule type: mRNA  
A/Residues: 1-117 <KLE>  
A/Cross-references: UNIPROT:P06309; UNIPARC:UPI000012E158  
A/Note: the sequence was determined from the differentiated gene  
C/Genetics:  
A/Gene: GDB:IGKV2

A/Cross-references: GDB:136265  
A/Map position: 2p12-2p12  
A/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
C/Superfamily: heterotetramer; immunoglobulin  
C/Keywords: heterotetramer; immunoglobulin  
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>  
F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>  
F:20-99/Domain: immunoglobulin homology <IMM>  
F:27-97/Disulfide bonds: #status predicted

Query Match 90.4%; Score 533.5; DB 1; Length 117;  
Best Local Similarity 92.0%; Pred. No. 1.3e-41;  
Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 60  
DB 5 DIVMTQSPSLPVTGPEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 64  
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113  
DB 65 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 116

## RESULT 8

S40356  
Ig kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40356  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40356  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-125 <KLE>  
A/Cross-references: UNIPARC:UPI000011616A; EMBL:X72466; NID:g441400; PIDN:CAA51134.1; PIDN:CAA51149.1; PIDN:CAA51143.0  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:25-104/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 532.5; DB 2; Length 125;  
Best Local Similarity 91.2%; Pred. No. 1.7e-41;  
Matches 103; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 60  
DB 10 DIVMTQSPSLPVTGPEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 69  
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113  
DB 70 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 121

## RESULT 9

K2HUTW  
Ig kappa chain V-II region (Tew) - human (tentative sequence)  
C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C/Accession: A90370; A92764; A01888  
R/Putnam, F.W.; Whitely Jr., E.J.; Paul, C.; Davidson, J.N.  
Biochemistry 12, 3763-3780, 1973  
A/Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloidosis.  
A/Reference number: A90370; MUID:74148480; PMID:4596149  
A/Contents: Bence Jones protein Tew  
A/Accession: A90370  
A/Molecule type: protein  
A/Residues: 1-113 <PUT>  
A/Cross-references: UNIPROT:P01617; UNIPARC:UPI0000012E157  
A/Note: this protein was isolated from the urine of a patient with plasma cell dyscrasia (multiple myeloma). The C region of this chain has the Inv (1,2) marker.  
R/Terry, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osseman, E.F.; Glenner, G.G.  
J. Clin. Invest. 52, 1276-1281, 1973  
A/Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient with amyloidosis.  
A/Reference number: A92764; MUID:73166638; PMID:4700495  
A/Contents: amyloid protein Tew  
A/Accession: A92764  
A/Molecule type: protein  
A/Residues: 1-27 <TER>  
A/Cross-references: UNIPARC:UPI00000173706  
A/Note: the major amyloid protein appears to be identical with the Bence Jones protein in amyloidosis.  
C/Genetics:  
A/Gene: GDB:IGKV2

A/Cross-references: GDB:136265  
A/Map position: 2p12-2p12  
A/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: amyloid; heterotetramer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>  
F:23-93/Disulfide bonds: #status predicted

Query Match 86.2%; Score 508.5; DB 1; Length 113;  
Best Local Similarity 86.7%; Pred. No. 2.3e-39;  
Matches 98; Conservative 11; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 60  
DB 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 60  
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113  
DB 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 112

## RESULT 10

S40371  
Ig kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40371  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40371  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-121 <KLE>  
A/Cross-references: UNIPARC:UPI0000116179; EMBL:X72481; NID:g441430; PIDN:CAA51149.1; PIDN:CAA51143.0  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:13-92/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 508.5; DB 2; Length 121;  
Best Local Similarity 90.0%; Pred. No. 2.5e-39;  
Matches 99; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 4 MTQSPSLPVTGPEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 63  
DB 1 MTQSPSLPVTGPEPASISCRSSQSLHNGYNYLDWYLOKPGQSPQLLIYLSNRA 60

```
QY 64 PDRFSGSGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113
|||||
Db 61 PDRFSSGSGTDTFTLKISRVEADVGYYCMQGLQT-PTTFGGTGLEIK 109
|||||

RESULT 11
S40372
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40372
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40372
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: UNIPARC:UPI000011617A; EMBL:X72482; NID:9441432; PIDN:CAA51150.1; PID:CAA51153.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 508.5; DB 2; Length 131;
Best Local Similarity 88.4%; Pred. No. 2.7e-39;
Matches 99; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYIGSNRA 60
|||||
Db 21 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYIGSTRA 80
|||||

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEI 112
|||||
Db 81 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQSPLOT-PYTFGGTGLEI 131
|||||

RESULT 12
S40319
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40319
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40319
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: UNIPARC:UPI0000116145; EMBL:X72429; NID:9441326; PIDN:CAA51097.1; PID:CAA51153.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-105/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 505; DB 2; Length 123;
Best Local Similarity 89.7%; Pred. No. 5.3e-39;
Matches 96; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYIGSNRA 60
|||||
Db 11 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYIGSNRA 70
|||||

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEI 107
|||||
Db 71 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQTPSVTSAGK 117
|||||

RESULT 13
S24681
Ig kappa chain - human
```

```
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S24681
R:van Es, J.H.
submitted to the EMBL Data Library, July 1992
A:Reference number: S24679
A:Accession: S24681
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <VAN>
A:Cross-references: UNIPARC:UPI00001160E1; EMBL:X67904; NID:933435; PIDN:CAA48102.1; PID:CAA48102.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 497; DB 2; Length 100;
Best Local Similarity 96.0%; Pred. No. 2.3e-38;
Matches 95; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYIGSNRA 60
|||||
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYIGSNRA 60
|||||

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEI 99
|||||
Db 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEI 99
|||||

RESULT 14
S40375
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40375
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40375
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-114 <KLE>
A:Cross-references: UNIPARC:UPI000011617D; EMBL:X72485; NID:9441438; PIDN:CAA51153.1; PID:CAA51153.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-92/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 487; DB 2; Length 114;
Best Local Similarity 89.4%; Pred. No. 2.1e-37;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 MTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYIGSNRAGV 63
|||||
Db 1 MTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYIGSNRAGV 60
|||||

QY 64 PDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEI 107
|||||
Db 61 PDRFSGSGGTDTFTLKISRVEADVGYYCMQALQTPSVTSAGK 104
|||||

RESULT 15
S03876
Ig kappa chain V-II region (Inc) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S03876
R:Perri, G.; Stoppani, M.; Iadarola, P.; Bellotti, V.; Merlini, G.
Biochim. Biophys. Acta 995, 103-108, 1989
A:Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.
A:Reference number: S03876; MUID:89194238; PMID:2495028
A:Accession: S03876
A:Molecule type: protein
A:Residues: 1-124 <PER>
```

A;Cross-references: UNIPARC:UPI000017679D  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>  
Query Match 81.9%; Score 483.5; DB 2; Length 124;  
Best Local Similarity 83.2%; Pred. No. 4.8e-37;  
Matches 94; Conservative 10; Mismatches 8; Indels 1; Gaps 1;  
Qy 1 DIVVTOSPLSLPVTGPEPASISCKSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLGSNRA 60  
Db 1 DIVVTOSPLSLPVTGPEPASISCKSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLGSNRA 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEADDDVGYVYCMQALQSLMCSFGQGTKEIK 113  
Db 61 SGVPDTFSGSGGTDFTLLISSLVGAEDEVGYVYCMQALQT-PWTFGGQTKVGIK 112

Search completed: April 25, 2007, 04:06:40  
Job time : 9.61864 secs

GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 77 Seconds  
(without alignments)  
1574.822 Million cell updates/sec

Title: US-10-665-383-40

Perfect score: 590

Sequence: 1 DIVMTQSPLEVTPEPAS.....MQALQSLMGCSFGQGTKLEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 8.4.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	533.5	90.4	117	1	KV2E_HUMAN	P06309 homo sapien
2	532.5	90.3	239	2	Q8NEK0_HUMAN	Q8NEK0 homo sapien
3	532	90.2	240	2	Q6FIH6_HUMAN	Q6FIH6 homo sapien
4	508.5	86.2	113	1	KV2D_HUMAN	P01617 homo sapien
5	481	81.5	112	1	KV2C_HUMAN	P01616 homo sapien
6	456	77.3	115	1	KV2A_HUMAN	P01614 homo sapien
7	450.5	76.4	113	1	KV2B_HUMAN	P01615 homo sapien
8	436.5	74.0	133	1	KV2F_HUMAN	P06310 homo sapien
9	436.5	74.0	248	2	Q6SZQ7_MOUSE	Q6SZQ7 mus sp. b3(
10	436	73.9	115	2	Q5F2I0_MOUSE	Q5F2I0 mus musculus
11	429.5	72.8	239	2	Q8TCD0_HUMAN	Q8TCD0 homo sapien
12	429.5	72.8	239	2	Q58E08_MOUSE	Q58E08 mus musculus
13	428.5	72.6	239	2	Q6P491_HUMAN	Q6P491 homo sapien
14	427	72.4	114	2	Q9UL80_HUMAN	Q9UL80 homo sapien
15	426.5	72.3	113	1	KV2G_MOUSE	P01631 mus musculus
16	418.5	70.9	219	2	Q6SZC0_MOUSE	Q6SZC0 mus musculus
17	416.5	70.6	113	1	KV2E_MOUSE	P03976 mus musculus
18	415.5	70.4	112	2	Q53VP8_MOUSE	Q53VP8 mus musculus
19	413.5	70.1	234	2	Q5XK94_MOUSE	Q5XK94 mus musculus
20	407.5	69.1	113	1	KV2F_MOUSE	P01630 mus musculus
21	406.5	68.9	112	1	KV2D_MOUSE	P01629 mus musculus
22	396.5	67.2	112	2	Q6LEM8_MOUSE	Q6LEM8 mus musculus
23	388.5	65.8	113	1	KV2C_MOUSE	P01628 mus musculus
24	388	65.8	108	1	KV1_CANFA	P01618 canis fami
25	386.5	65.5	112	1	KV2A_MOUSE	P01626 mus musculus
26	380	64.4	114	1	KV4A_HUMAN	P01625 homo sapien
27	373	63.2	120	1	KV2B_MOUSE	P01627 mus musculus
28	372	63.1	134	1	KV4C_HUMAN	P06314 homo sapien
29	365.5	61.9	133	1	KV4B_HUMAN	P06313 homo sapien
30	361	61.2	255	2	Q6KB05_MOUSE	Q6KB05 mus musculus
31	355.5	60.3	109	1	KV3E_HUMAN	P01623 homo sapien

32	354	60.0	240	2	Q52L64_MOUSE	Q52L64 mus musculus
33	352.5	59.7	109	1	KV3B_HUMAN	P01620 homo sapien
34	352.5	59.7	109	1	KV3D_HUMAN	P01622 homo sapien
35	349	59.2	236	2	Q6PII8_HUMAN	Q6PII8 homo sapien
36	348.5	59.1	129	1	KV3L_HUMAN	P18135 homo sapien
37	347.5	58.9	129	1	KV3M_HUMAN	P18136 homo sapien
38	345.5	58.6	109	2	Q9UL78_HUMAN	Q9UL78 homo sapien
39	345	58.5	111	1	KV3S_MOUSE	P01671 mus musculus
40	345	58.5	111	2	Q920E9_MOUSE	Q920E9 mus musculus
41	344	58.3	111	1	KV3R_MOUSE	P01670 mus musculus
42	344	58.3	111	1	KV3U_MOUSE	P01673 mus musculus
43	342.5	58.1	109	1	KV3G_HUMAN	P04206 homo sapien
44	340.5	57.7	235	2	Q6GMW0_HUMAN	Q6GMW0 homo sapien
45	338.5	57.4	108	1	KV3A_HUMAN	P01619 homo sapien

#### ALIGNMENTS

RESULT 1						
KV2E_HUMAN						
ID KV2E_HUMAN	STANDARD;	PRT;	117 AA.			
AC P06309;						
DT 01-JAN-1988,	integrated into UniProtKB/Swiss-Prot.					
DT 01-JAN-1988,	sequence version 1.					
DT 27-JUN-2006,	entry version 47.					
DE Ig kappa chain V-II region	GM607 precursor (Fragment).					
OS Homo sapiens (Human).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;						
OC Catarrhini; Hominidae; Homo.						
OX NCBI_TaxID:9606;						
RN [1]						
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].						
RX MEDLINE:84191506; PubMed:6325927; DOI=10.1038/309073a0;						
RA Klobbeck H.G., Solomon A., Zachau H.G.;						
RT "Contribution of human V kappa II germ-line genes to light-chain						
RT diversity."						
RL Nature 309:73-76(1984).						
CC						
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CC						
CC EMEL; Z00009; -; NOT_ANNOTATED_CDS; Genomic_DNA.						
DR PIR; A01889; K2HUGM.						
DR HSSP; Q99M37; 1191.						
DR SNR; P06309; 5-115.						
DR LinkHub; P06309; -.						
DR GO; GO:0005576; C:extracellular region; NAS.						
DR GO; GO:0003823; F:antigen binding; NAS.						
DR GO; GO:0006955; P:immune response; NAS.						
DR InterPro; IPR007110; Ig-like.						
DR InterPro; IPR003599; Ig sub.						
DR InterPro; IPR013106; Ig_V-set.						
DR InterPro; IPR003596; Ig_V-set_sub.						
DR Pfam; PF07686; V-set; 1.						
DR SMART; SM00409; IG; 1.						
DR SMART; SM00406; IG; 1.						
DR PROSITE; PS50835; IG LIKE; 1.						
KW Immunoglobulin domain; Immunoglobulin V region; Signal.						
FT SIGNAL	<1	4				
FT CHAIN	5	117				
FT REGION	5	27				
FT REGION	28	43				
FT REGION	44	58				
FT REGION	59	65				
FT REGION	66	96				
FT REGION	98	106				
FT REGION	107	116				
FT DISULFID	27	97				
FT NON_TER	1	1				
FT NON_TER	117	117				

Ig kappa chain V-II region GM607.  
/FTID=PRO\_0000015172.  
Framework-1.  
Complementarity-determining-1.  
Framework-2.  
Complementarity-determining-2.  
Framework-3.  
Complementarity-determining-3.  
Framework-4.  
By similarity.









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RN  PROTEIN SEQUENCE.
RX  MEDLINE=76253627; PubMed=821524;
RA  Riesen W.F., Jaton J.-C.;
RT  "Variable region sequence of the light chain from a Waldenstroms IgM
RL  with specificity for phosphorylcholine.";
RL  Biochemistry 15:3829-3833(1976).
CC  -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC  macroglobulin that binds phosphorylcholine.
CC  -----
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CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  PIR; A01886; K2HURF.
DR  HSSP; Q99M37; 1191.
DR  SMR; P01615; 1-109.
DR  GO; GO:0005576; C:extracellular region; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003599; Ig_sub.
DR  InterPro; IPR013106; Ig_V-set.
DR  InterPro; IPR003596; Ig_V-set_sub.
DR  Pfam; PF07686; V-set; 1.
DR  SMART; SM00409; IG; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS00835; IG LIKE; 1.
KW  Direct protein sequencing; Immunoglobulin domain;
KW  Immunoglobulin V region.
FT  CHAIN 1 >113
FT  REGION 1 23
FT  REGION 24 39
FT  REGION 40 54
FT  REGION 55 61
FT  REGION 62 93
FT  REGION 94 102
FT  REGION 103 112
FT  REGION 112 93
FT  DISULFID 23 93
FT  NON_TER 113 113
SQ  SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 76.4%; Score 450.5; DB 1; Length 113;
Best Local Similarity 77.0%; Pred. No. 2.4e-40;
Matches 87; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVMTQSPPLSPVTGPEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPOLLILYGSNRA 60
Db 1 DVVMTQSPPLFLPTLGEPAISIQCRSSQSLVRYRGTYLWYLQKPGQSPOLLILYSSYRD 60

QY 61 SGVPRFSGSGSGTDFTLKISRVEADPGVYVCMQALQSLMCSFGQGTGLEIK 113
Db 61 SGVPRFSGSGSGTDFTLKISRVEADPGVYVCMQATZS-PYTFGGGTGLZIK 112

RESULT 8
KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1988, sequence version 1.
DT 30-MAY-2006, entry version 43.
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Eutheria; Euarchoptogires; Primates; Haplorhini;
OC Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combrinato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
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III.";
Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
DR EMBL; Z00020; CAA77315.1; -; Genomic_DNA.
DR PIR; A01890; K2HURF.
DR HSSP; Q99M37; 1191.
DR SMR; P06310; 21-133.
DR Ensembl; ENSG00000173758; Homo sapiens.
DR LinkHub; P06310; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
KW Immunoglobulin V region.
FT CHAIN 1 20
FT CHAIN 21 133
FT REGION 21 43
FT REGION 44 59
FT REGION 60 74
FT REGION 75 81
FT REGION 82 113
FT REGION 114 122
FT REGION 123 132
FT REGION 132 133
FT DISULFID 43 113
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 74.0%; Score 436.5; DB 1; Length 133;
Best Local Similarity 76.1%; Pred. No. 9.4e-39;
Matches 86; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 DIVMTQSPPLSPVTGPEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPOLLILYGSNRA 60
Db 21 DVVMTQSPPLSPVTLPQAPASISCRSSQSLVSDNTYLNWFQQRPGQSPRLIYKVSNRD 80

QY 61 SGVPRFSGSGSGTDFTLKISRVEADPGVYVCMQALQSLMCSFGQGTGLEIK 113
Db 81 SGVPRFSGSGSGTDFTLKISRVEADPGVYVCMQGTTH-WSWTFGGGTKEIK 132

RESULT 9
Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 18-APR-2006, entry version 11.
DE B3(Fv)-PE40 (Fragment).
GN Name=B3 (Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchoptogires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
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DR EMBL; S57990; AAB19971.2; -; mRNA.  
DR SMR; Q65207; 4-247.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig sub.  
DR InterPro; IPR013106; Ig V-set.  
DR InterPro; IPR003596; Ig V-set\_sub.  
DR Pfam; PF07686; V-set; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG LIKE; 2.  
KW Immunoglobulin domain.  
FT NON\_TER 248 248  
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43B570950 CRC64;

Query Match 74.0%; Score 436.5; DB 2; Length 248;  
Best Local Similarity 75.2%; Pred. No. 2e-38;  
Matches 85; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 1 DIVMTQSLPLSVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIIYLGSNRA 60  
DB 136 DVLMTQSLPLSVSLGDAQSISCRSSQIIVHSHNGYNYLDWYLOKPGQSPKLLIYKVSNR 195  
QY 61 SGVPRFSGSGSGTDFTLKISRVEADDGVVYVCMQALQSLMCSFGQGTGLEIK 113  
DB 196 SGVPRFSGSGSGTDFTLKISRVEADDGVVYVCMQALQSLMCSFGQGTGLEIK 247

## RESULT 10

QSF210\_MOUSE  
ID QSF210\_MOUSE PRELIMINARY; PRT; 115 AA.  
AC QSF210;  
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.  
DT 11-JUN-2005, sequence version 1.  
DT 11-JUL-2006, entry version 8.  
DE Kappa light chain variable region (Fragment).  
GN Name=IgG1 anti-TS1 VL;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22716456; PubMed=12833571; DOI=10.1002/jmr.617;  
RA Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;  
RT "Studies of the interactions between the anticytokerin 8 monoclonal  
RT antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1.";  
RL J. Mol. Recognit. 16:157-163(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Erlandsson A.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AJ884575; CAI56337.1; -; mRNA.  
DR SMR; QSF210; 1-115.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig sub.  
DR InterPro; IPR013106; Ig V-set.  
DR InterPro; IPR003596; Ig V-set\_sub.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin domain.  
FT NON\_TER 1 115  
SQ SEQUENCE 115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;

Query Match 73.9%; Score 436; DB 2; Length 115;  
Best Local Similarity 75.2%; Pred. No. 8.9e-39;  
Matches 85; Conservative 11; Mismatches 17; Indels 0; Gaps 0;  
QY 1 DIVMTQSLPLSVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIIYLGSNRA 60  
DB 1 DVVMTQTPLSLFVSLGDAQSISCRSSQSLVHSHNGYNYLDWYLOKPGQSPKLLIYKVSNR 60  
QY 61 SGVPRFSGSGSGTDFTLKISRVEADDGVVYVCMQALQSLMCSFGQGTGLEIK 113  
DB 61 SGVPRFSGSGSGTDFTLKISRVEADDGVVYVCMQALQSLMCSFGQGTGLEIK 113

## RESULT 11

Q8TCD0\_HUMAN  
ID Q8TCD0\_HUMAN PRELIMINARY; PRT; 239 AA.  
AC Q8TCD0;  
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2002, sequence version 1.  
DT 27-JUN-2006, entry version 29.  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
OC Catarrhini; Hominoidea; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92285150; PubMed=1598223;  
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;  
RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus  
RT nephritis-associated idiotype.";  
RL Nucleic Acids Res. 20:2601-0(1992).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92201291; PubMed=1551402;  
RA Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,  
RA Thiebe R., Zocher I., Zachau H.G.;  
RT "The human immunoglobulin kappa locus. Characterization of the  
RT duplicated A regions.";  
RL Eur. J. Immunol. 22:1023-1029(1992).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.



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RESULT 13
Q6P491 HUMAN
ID Q6P491_HUMAN PRELIMINARY; PRT; 239 AA.
AC Q6P491;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 27-JUN-2006, entry version 22.
DE Hypothetical protein LOC651928.
GN Name=LOC651928;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenker C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny E., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC NIH MGC Project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL; BC063599; AAH63599.1; -; mRNA.
CC HSSP; P01837; 1KCU.
CC SMR; O6P491; 21-237.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0006020; C:membrane; IEA.
CC GO; GO:0030106; F:MHC class I receptor activity; IEA.
CC GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
CC GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; IEA.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_C1-set.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003599; Ig_sub.
CC InterPro; IPR013106; Ig_V-set.
CC InterPro; IPR003596; Ig_V-set_sub.
CC Pfam; PF07654; C1-set; 1.
CC Pfam; PF07686; V-set; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00407; IGc1; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 2.
CC PROSITE; PS00290; IG_MHC; UNKNOWN 1.
CC Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
KW
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KW Transmembrane.
SQ SEQUENCE 239 AA; 26246 MW; 26246 MW; CD7313DDFFD358B3 CRC64;
Query Match 72.6%; Score 428.5; DB 2; Length 239;
Best Local Similarity 75.2%; Pred. No. 1.4e-37;
Matches 85; Conservative 11; Mismatches 16; Indels 1; Gaps 1;
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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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ID Q9UL80_HUMAN PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RT Clin. Immunol. Immunopathol. 87:184-192 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=92352481; PubMed=1322670;
RA Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,
RA Gaskin F., Fu S.M.;
RT "A rheumatoid factor from a normal individual encoded by VH2 and V
RT kappa II gene segments."
RL Arthritis Rheum. 35:900-904 (1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation."
RL Eur. J. Immunol. 23:391-397 (1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=92289816; PubMed=1601042;
RA Huber C., Klobbeck H.G., Zachau H.G.;
RT "Ongoing V kappa-J kappa recombination after formation of a productive
RT V kappa-J kappa coding joint."
RL Eur. J. Immunol. 22:1561-1565 (1992).
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL; AF035034; AAD56270.1; -; mRNA.
CC PIR; B49002; B49002.
CC PIR; S23638; S23638.
CC PIR; S34094; S34094.
CC PIR; S34095; S34095.
CC HSSP; P01625; ILVE.
CC SMR; Q9UL80; 1-114.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig_sub.
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DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
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DR PROSITE; PS00835; IG_LIKE; 1.
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Best Local Similarity 74.3%; Pred. No. 8.2e-38;
Matches 84; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

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QY 61 SGVDPDFSGSGGTDTFTLKISRVEADVGYYCMAQLQSLMCSFGQGTKLEIK 113
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ID KV2G_MOUSE STANDARD; PRT; 113 AA.
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DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 30-MAY-2006, entry version 40.
DE IG kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RT anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
CC protein that binds digoxin.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC PIR; A01914; KVM526.
CC HSP; Q99M37; I191.
CC Ensembl; ENSMUSG000005315; Mus musculus.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig_sub.
CC InterPro; IPR013106; Ig_V-set.
CC Pfam; PF07686; V-set; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00406; IG; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
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FT CHAIN 1 >113
FT REGION 1 23
FT REGION 24 39
FT REGION 40 54
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FT REGION 62 93
FT REGION 94 102
FT REGION 103 112
FT Framework-1.
FT Framework-2.
FT Framework-3.
FT Framework-4.
FT Complementarity-determining-1.
FT Complementarity-determining-2.
FT Complementarity-determining-3.
FT Complementarity-determining-4.
FT Framework-1.
FT Framework-2.
FT Framework-3.
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FT Complementarity-determining-2.
FT Complementarity-determining-3.
FT Complementarity-determining-4.
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FT NON TER 113 113
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Query Match 72.3%; Score 426.5; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 9.2e-38;
Matches 84; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 DIVMTQSPVLSPLPTPGEPASISCRSSQSLHSHNGYNLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DVVMTQSPVLSPLPTVLRQPAISICRSPVSDGNLYLNWFQORPGQSPRLIYKVSNR 60

QY 61 SGVDPDFSGSGGTDTFTLKISRVEADVGYYCMAQLQSLMCSFGQGTKLEIK 113
DB 61 SGVDPDFSGSGGTDTFTLKISRVEADVGYYCMAQGTHTWPPWTFGGQTKLEIK 113

Search completed: April 25, 2007, 04:06:36
Job time : 77.9294 secs
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GenCore version 6.2.1  
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:06:51 ; Search time 14 Seconds  
(without alignments)  
696.311 Million cell updates/sec

Title: US-10-665-383-40

Perfect score: 590

Sequence: 1 DIWMTQSPLSLVPTFCPEAS.....MOALQSLMCSFGQTKLEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pcp:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pcp:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB.pcp:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS COMB.pcp:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pcp:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	547.5	92.8	113	2	US-09-025-769B-15
2	547.5	92.8	113	2	US-09-490-070A-15
3	547.5	92.8	113	2	US-09-490-153-15
4	547.5	92.8	113	2	US-09-490-324-15
5	544.5	92.3	112	2	US-09-254-180C-9
6	533.5	90.4	112	1	US-08-331-398A-49
7	533.5	90.4	112	1	US-08-331-397B-49
8	533.5	90.4	112	1	US-08-759-804A-49
9	533.5	90.4	112	2	US-09-227-693-49
10	530.5	89.9	112	2	US-10-330-613A-2
11	521.5	88.4	114	2	US-09-025-769B-29
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13	521.5	88.4	114	2	US-09-490-070A-29
14	521.5	88.4	114	2	US-09-490-070A-45
15	521.5	88.4	114	2	US-09-490-153-29
16	521.5	88.4	114	2	US-09-490-153-45
17	521.5	88.4	114	2	US-09-490-324-29
18	521.5	88.4	114	2	US-09-490-324-45
19	521.5	88.4	281	2	US-09-025-769B-178
20	521.5	88.4	281	2	US-09-490-070A-178
21	521.5	88.4	281	2	US-09-490-153-178
22	521.5	88.4	281	2	US-09-490-324-178
23	520.5	88.2	113	1	US-08-082-623-4
24	519.5	88.1	112	1	US-10-330-613A-38
25	512.5	86.9	112	1	US-08-053-171-16
26	510	86.4	100	2	US-09-472-087-115

27	510	86.4	100	2	US-10-194-975-79	Sequence 79, Appl
28	510	86.4	100	2	US-10-194-975-80	Sequence 80, Appl
29	510	86.4	100	2	US-10-330-613A-71	Sequence 71, Appl
30	505.5	85.7	112	2	US-09-000-088-2	Sequence 2, Appl
31	502.5	85.2	112	2	US-09-240-274-30	Sequence 30, Appl
32	502.5	85.2	112	2	US-09-848-798-30	Sequence 30, Appl
33	499.5	84.7	112	1	US-08-478-039-88	Sequence 88, Appl
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36	499.5	84.7	239	2	US-09-992-095B-8	Sequence 8, Appl
37	499.5	84.7	239	3	US-10-000-986A-8	Sequence 8, Appl
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39	494.5	83.8	108	1	US-08-477-484B-151	Sequence 151, App
40	494.5	83.8	108	1	US-08-107-669D-15	Sequence 15, Appl
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42	494.5	83.8	108	1	US-08-477-531B-15	Sequence 15, Appl
43	494.5	83.8	108	1	US-08-646-360-151	Sequence 151, App
44	494.5	83.8	108	1	US-08-082-842A-15	Sequence 15, Appl
45	494.5	83.8	108	2	US-08-839-765-151	Sequence 151, App

#### ALIGNMENTS

RESULT 1  
US-09-025-769B-15  
; Sequence 15, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthum, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA: US/09/025,769B  
; APPLICATION NUMBER: 18-FEB-1998  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-15  
Query Match 92.8%; Score 547.5; DB 2; Length 113;  
Best Local Similarity 94.7%; Pred. No. 1.3e-46;

Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSGNGNYLDWYLOKPGQSPQLLIYLGSNRA 60  
 Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSGNGNYLDWYLOKPGQSPQLLIYLGSNRA 60  
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RESULT 2

US-09-490-070A-15  
 ; Sequence 15, Application US/09490070A  
 ; Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim  
 Pack, Peter  
 Ilag, Vic  
 Ge, Liming  
 Moroney, Simon  
 Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
 White & McAlliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-490-070A-15

Query Match 92.8%; Score 547.5; DB 2; Length 113;

Best Local Similarity 94.7%; Pred. No. 1.3e-46;

Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSGNGNYLDWYLOKPGQSPQLLIYLGSNRA 60

Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSGNGNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 113

Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 112

RESULT 3

US-09-490-153-15

; Sequence 15, Application US/09490153

; Patent No. 6706484

GENERAL INFORMATION:

APPLICANT: Knappik, Achim  
 Pack, Peter  
 Ilag, Vic  
 Ge, Liming  
 Moroney, Simon  
 Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-490-153-15

Query Match 92.8%; Score 547.5; DB 2; Length 113;

Best Local Similarity 94.7%; Pred. No. 1.3e-46;

Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSGNGNYLDWYLOKPGQSPQLLIYLGSNRA 60

Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSGNGNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 113

Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 112

RESULT 4

US-09-490-324-15

; Sequence 15, Application US/09490324

; Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim  
 Pack, Peter  
 Ilag, Vic  
 Ge, Liming  
 Moroney, Simon

```
/ Plueckthun, Andreas
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
/ STREET: 1251 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10021
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/490,324
/ FILING DATE: 24-Jan-2000
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,769
/ FILING DATE: 18-FEB-1998
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-324-15

Query Match          92.8%; Score 547.5; DB 2; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.3e-46;
Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVWTQSLPLVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLSNRA 60
DB 1 DIVWTQSLPLVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLSNRA 60
QY 61 SGVDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGGQTKLEIK 113
DB 61 SGVDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQ-T-PYTFGGQTKLEIK 112

RESULT 5
US-09-254-180C-9
/ Sequence 9, Application US/09254180C
/ Patent No. 6777540
/ GENERAL INFORMATION:
/ APPLICANT: OKUMURA, KO
/ APPLICANT: OKUMURA, KO
/ APPLICANT: ED A. Yasuyuki
/ APPLICANT: MAEDA, Hiroaki
/ APPLICANT: USHIO, Yoshitaka
/ APPLICANT: HIGUCHI, Hirofumi
/ APPLICANT: NAKATA, Motomi
/ TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
/ TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
/ FILE REFERENCE: 050006-0055
/ CURRENT APPLICATION NUMBER: US/09/254,180C
/ CURRENT FILING DATE: 1999-04-15
/ PRIOR APPLICATION NUMBER: PCT/JP97/02983
/ PRIOR FILING DATE: 1997-08-27
/ PRIOR APPLICATION NUMBER: 271546/1996
/ PRIOR FILING DATE: 1996-09-20
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/ PRIOR APPLICATION NUMBER: 231472/1996
/ PRIOR FILING DATE: 1996-09-02
/ NUMBER OF SEQ ID NOS: 183
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-254-180C-9

Query Match          92.3%; Score 544.5; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 2.6e-46;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVWTQSLPLVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLSNRA 60
DB 1 DIVWTQSLPLVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLSNRA 60
QY 61 SGVDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGGQTKLEIK 113
DB 61 SGVDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQ-T-PYTFGGQTKLEIK 112

RESULT 6
US-08-331-398A-49
/ Sequence 49, Application US/08331398A
/ Patent No. 5608039
/ GENERAL INFORMATION:
/ APPLICANT: Pastan, Ira
/ APPLICANT: Willingham, Mark
/ APPLICANT: FitzGerald, David
/ APPLICANT: Brinkmann, Ulrich
/ APPLICANT: Pai, Lee
/ TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
/ TITLE OF INVENTION: and Their Uses (as amended)
/ NUMBER OF SEQUENCES: 68
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew
/ STREET: One Market Plaza, Steuart Street Plaza
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/331,398A
/ FILING DATE: 28-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/767,331
/ FILING DATE: 30-SEP-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/596,289
/ FILING DATE: 12-OCT-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 015280-126110US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 543-9600
/ TELEFAX: (415) 543-5043
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 112 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
```

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/ NAME/KEY: Protein
/ LOCATION: 1..112
/ OTHER INFORMATION: /note="Human IgM antibody GM607
/ OTHER INFORMATION: Variable Light Chain (V-L)"
US-08-331-397B-49

Query Match          90.4%; Score 533.5; DB 1; Length 112;
Best Local Similarity 92.0%; Pred. No. 3.1e-45;
Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPPLSLPTGEPASISCRSSQSLHSHNGNYLDWYLOKPGQSPQLLIYIGSNRA 60
DB 1 DIVMTQSPPLSLPTGEPASISCRSSQSLHSHNGNYLDWYLOKPGQSPQLLIYIGSNRA 60
QY 61 SGVPRFSGSGGTFTLKISRVEADDDGVVYCMQALQSLMCSFGGQTKLEIK 113
DB 61 SGVPRFSGSGGTFTLKISRVEADDDGVVYCMQALQSLMCSFGGQTKLEIK 112

RESULT 7
US-08-331-397B-49
/ Sequence 49, Application US/08331397B
/ Patent No. 5981726
/ GENERAL INFORMATION:
/ APPLICANT: Pastan, Ira
/ APPLICANT: Benhar, Itai
/ TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
/ TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
/ TITLE OF INVENTION: Thereof
/ NUMBER OF SEQUENCES: 68
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew
/ STREET: One Market Plaza, Stewart Street Plaza
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/331,397B
/ FILING DATE: 28-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/767,331
/ FILING DATE: 30-SEP-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/596,289
/ FILING DATE: 12-OCT-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 015280-126120US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 543-9600
/ TELEFAX: (415) 543-5043
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 112 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Protein
/ LOCATION: 1..112
/ OTHER INFORMATION: /note="Human IgM antibody GM607
/ OTHER INFORMATION: Variable Light Chain (V-L)"
US-08-331-397B-49
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Query Match          90.4%; Score 533.5; DB 1; Length 112;
Best Local Similarity 92.0%; Pred. No. 3.1e-45;
Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPPLSLPTGEPASISCRSSQSLHSHNGNYLDWYLOKPGQSPQLLIYIGSNRA 60
DB 1 DIVMTQSPPLSLPTGEPASISCRSSQSLHSHNGNYLDWYLOKPGQSPQLLIYIGSNRA 60
QY 61 SGVPRFSGSGGTFTLKISRVEADDDGVVYCMQALQSLMCSFGGQTKLEIK 113
DB 61 SGVPRFSGSGGTFTLKISRVEADDDGVVYCMQALQSLMCSFGGQTKLEIK 112

RESULT 8
US-08-759-804A-49
/ Sequence 49, Application US/08759804A
/ Patent No. 5990296
/ GENERAL INFORMATION:
/ APPLICANT: Pastan, Ira
/ APPLICANT: Willingham, Mark
/ APPLICANT: Fitzgerald, David J.
/ APPLICANT: Brinkmann, Ulrich
/ APPLICANT: Pai, Lee
/ TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
/ TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
/ NUMBER OF SEQUENCES: 68
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/759,804A
/ FILING DATE: 03-DEC-1996
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/331,398
/ FILING DATE: 28-OCT-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/767,331
/ FILING DATE: 30-SEP-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/596,289
/ FILING DATE: 12-OCT-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Weber, Ellen L.
/ REGISTRATION NUMBER: 32,762
/ REFERENCE/DOCKET NUMBER: 015280-126140US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 112 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Protein
/ LOCATION: 1..112
/ OTHER INFORMATION: /note="Human IgM antibody GM607
/ OTHER INFORMATION: Variable Light Chain (V-L)"
US-08-759-804A-49

Query Match          90.4%; Score 533.5; DB 1; Length 112;
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Best Local Similarity 92.0%; Pred. No. 3.1e-45;  
Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60

Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113

Db 61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 112

## RESULT 9

US-09-227-693-49

; Sequence 49, Application US/09227693

; Patent No. 6287562

; GENERAL INFORMATION:

; APPLICANT: PASTAN, Ira

; APPLICANT: BENHAR, Itai

; APPLICANT: PADLAN, Eduardo A.

; APPLICANT: JUNG, Sun-Hee

; APPLICANT: LEE, Byungkook

; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY

; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: Stuart Street Tower, One Market Plaza

; CITY: San Francisco

; STATE: California

; COUNTRY: US

; ZIP: 94105-1493

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/227,693

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/331,396

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/767,331

; FILING DATE: 30-SEP-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/596,289

; FILING DATE: 12-OCT-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 15280-126-1-3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 543-9600

; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..112

; OTHER INFORMATION: /note="Human IgM GM607 VL region"

US-09-227-693-49

Query Match

Best Local Similarity 90.4%; Score 533.5; DB 2; Length 112;

Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60

Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113

Db 61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 112

## RESULT 10

US-10-330-613A-2

; Sequence 2, Application US/10330613A

; Patent No. 6924360

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

; FILE REFERENCE: ABGENIX.022A

; CURRENT APPLICATION NUMBER: US/10/330.613A

; PRIOR FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: 60/346299

; PRIOR FILING DATE: 2001-12-18

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-330-613A-2

Query Match 89.9%; Score 530.5; DB 2; Length 112;

Best Local Similarity 92.0%; Pred. No. 6.2e-45;

Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60

Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113

Db 61 SGVPDRFSGSGGTDFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 112

## RESULT 11

US-09-025-769B-29

; Sequence 29, Application US/09025769B

; Patent No. 6300064

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Pack, Peter

; APPLICANT: Ilag, Vic

; APPLICANT: Ge, Liming

; APPLICANT: Moroney, Simon

; APPLICANT: Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-29

Query Match 88.4%; Score 521.5; DB 2; Length 114;  
Best Local Similarity 90.3%; Pred. No. 4.8e-44;  
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60  
Db 1 DIVMTQSPSLSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFRSGSGSDFTLKISRVEADDDGVYVYCMQALQSLMCSFGQGTKEIK 113  
Db 61 SGVPRFRSGSGSDFTLKISRVEADDDGVYVYCMQALQSLMCSFGQGTKEIK 112

RESULT 12  
US-09-025-769B-45  
Sequence 45, Application US/09025769B  
Patent No. 630064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

QY 1 DIVMTQSPSLSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60  
Db 1 DIVMTQSPSLSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFRSGSGSDFTLKISRVEADDDGVYVYCMQALQSLMCSFGQGTKEIK 113  
Db 61 SGVPRFRSGSGSDFTLKISRVEADDDGVYVYCMQALQSLMCSFGQGTKEIK 112

RESULT 13  
US-09-490-070A-29  
Sequence 29, Application US/09490070A  
Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-490-070A-29

Query Match 88.4%; Score 521.5; DB 2; Length 114;  
Best Local Similarity 90.3%; Pred. No. 4.8e-44;  
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60  
Db 1 DIVMTQSPSLSPVTPGEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFRSGSGSDFTLKISRVEADDDGVYVYCMQALQSLMCSFGQGTKEIK 113

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Db      61  SGVPRFSGSGGTDFTLKISRVEADVGYYCQOH-YTTPTFGGTKVEIK 112
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RESULT 14
US-09-490-070A-45
; Sequence 45, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-490-070A-45
Query Match      88.4%; Score 521.5; DB 2; Length 114;
Best Local Similarity 90.3%; Pred. No. 4.8e-44;
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY      1  DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRA 60
|||||
Db      1  DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRA 60
|||||
QY      61  SGVPRFSGSGGTDFTLKISRVEADVGYYCQOH-YTTPTFGGTKVEIK 113
|||||
Db      61  SGVPRFSGSGGTDFTLKISRVEADVGYYCQOH-YTTPTFGGTKVEIK 112
|||||

RESULT 15
US-09-490-153-29
; Sequence 29, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-490-153-29
Query Match      88.4%; Score 521.5; DB 2; Length 114;
Best Local Similarity 90.3%; Pred. No. 4.8e-44;
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY      1  DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRA 60
|||||
Db      1  DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRA 60
|||||
QY      61  SGVPRFSGSGGTDFTLKISRVEADVGYYCQOH-YTTPTFGGTKVEIK 113
|||||
Db      61  SGVPRFSGSGGTDFTLKISRVEADVGYYCQOH-YTTPTFGGTKVEIK 112
|||||

Search completed: April 25, 2007, 04:08:32
Job time : 15.2048 secs

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GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 42 Seconds  
(without alignments)  
1251.741 Million cell updates/sec

Title: US-10-665-383-40

Perfect score: 590

Sequence: 1 DIVMTOSPLSLVPTGEPAS.....MQALQSLMCSFGQGTGLEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:\*
- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
  - 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
  - 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
  - 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
  - 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	590	100.0	113	4	US-10-041-860-30		Sequence 30, Appl
2	590	100.0	113	4	US-10-041-860-221		Sequence 221, App
3	590	100.0	113	4	US-10-041-860-255		Sequence 255, App
4	590	100.0	113	4	US-10-665-383-40		Sequence 40, Appl
5	576.5	97.7	114	4	US-10-041-860-322		Sequence 322, App
6	554	93.9	113	6	US-11-021-715-89		Sequence 89, Appl
7	550	93.2	112	5	US-10-726-332-215		Sequence 215, App
8	549	93.1	113	6	US-11-021-715-88		Sequence 88, Appl
9	548.5	93.0	110	4	US-10-309-762-165		Sequence 165, App
10	547.5	92.8	112	6	US-11-021-715-74		Sequence 74, Appl
11	547.5	92.8	112	6	US-10-292-088-104		Sequence 104, App
12	547.5	92.8	112	6	US-11-021-715-75		Sequence 75, Appl
13	547.5	92.8	112	6	US-11-021-715-92		Sequence 92, Appl
14	547.5	92.8	113	5	US-10-834-397-15		Sequence 15, Appl
15	547	92.7	112	5	US-10-726-332-24		Sequence 24, Appl
16	546.5	92.6	112	6	US-11-021-715-77		Sequence 77, Appl
17	546.5	92.6	134	5	US-10-858-855-8		Sequence 8, Appl
18	546	92.5	111	5	US-10-727-155-276		Sequence 276, App
19	546	92.5	112	5	US-10-725-962-42		Sequence 42, Appl
20	545.5	92.5	112	5	US-10-735-916A-58		Sequence 58, Appl
21	545.5	92.5	112	6	US-11-012-353-58		Sequence 58, Appl
22	545.5	92.5	113	4	US-10-308-817-177		Sequence 177, App
23	545.5	92.5	113	4	US-10-453-698-177		Sequence 177, App
24	544.5	92.3	112	4	US-10-292-088-103		Sequence 103, App
25	544.5	92.3	112	4	US-10-292-088-111		Sequence 111, App
26	544.5	92.3	112	5	US-10-877-773-30		Sequence 30, Appl
27	544.5	92.3	112	5	US-10-877-774-30		Sequence 30, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-041-860-30  
; Sequence 30, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gad  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: ABGENIX.051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-30

Query Match 100.0%; Score 590; DB 4; Length 113;  
Best Local Similarity 100.0%; Pred. No. 4.3e-46;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIVMTOSPLSLVPTGEPASISCRSSQSLHSGNYLDWYLOKPGOSPQLIYLGSNRA	60
DB	1	DIVMTOSPLSLVPTGEPASISCRSSQSLHSGNYLDWYLOKPGOSPQLIYLGSNRA	60
QY	61	SGVPRFSGSGSGTDTFTLKISRVEADDDVGVYVCMQALQSLMCSFGQGTGLEIK	113
DB	61	SGVPRFSGSGSGTDTFTLKISRVEADDDVGVYVCMQALQSLMCSFGQGTGLEIK	113

##### RESULT 2

US-10-041-860-221  
; Sequence 221, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gad



```

; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 113
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-221

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Query Match      100.0%; Score 590; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.3e-46;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNLYDWYLOKPGQSPQLLIYLGNSRA 60
Db 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNLYDWYLOKPGQSPQLLIYLGNSRA 60

QY 61 SGVDPDRFSGSGGTDFTLKISRVEADDDGYYVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVDPDRFSGSGGTDFTLKISRVEADDDGYYVYCMQALQSLMCSFGQGTKEIK 113

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RESULT 3
US-10-041-860-255
; Sequence 255, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255
; LENGTH: 113
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-255

```

```

Query Match      100.0%; Score 590; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.3e-46;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNLYDWYLOKPGQSPQLLIYLGNSRA 60
Db 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNLYDWYLOKPGQSPQLLIYLGNSRA 60

QY 61 SGVDPDRFSGSGGTDFTLKISRVEADDDGYYVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVDPDRFSGSGGTDFTLKISRVEADDDGYYVYCMQALQSLMCSFGQGTKEIK 113

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RESULT 4
US-10-665-383-40
; Sequence 40, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen

```

```

; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 113
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-40

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```

Query Match      100.0%; Score 590; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.3e-46;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNLYDWYLOKPGQSPQLLIYLGNSRA 60
Db 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNLYDWYLOKPGQSPQLLIYLGNSRA 60

QY 61 SGVDPDRFSGSGGTDFTLKISRVEADDDGYYVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVDPDRFSGSGGTDFTLKISRVEADDDGYYVYCMQALQSLMCSFGQGTKEIK 113

```

```

RESULT 5
US-10-041-860-322
; Sequence 322, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 322
; LENGTH: 114
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-322

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```

Query Match      97.7%; Score 576.5; DB 4; Length 114;
Best Local Similarity 98.2%; Pred. No. 7.4e-45;
Matches 112; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNLYDWYLOKPGQSPQLLIYLGNSRA 60
Db 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHNSGYNLYDWYLOKPGQSPQLLIYLGNSRA 60

QY 61 SGVDPDRFSGSGGTDFTLKISRVEADDDGYYVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVDPDRFSGSGGTDFTLKISRVEADDDGYYVYCMQALQSLMCSFGQGTKEIK 114

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```

RESULT 6
US-11-021-715-89

```

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; Sequence 89, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-89

Query Match          93.9%; Score 554; DB 6; Length 113;
Best Local Similarity 93.8%; Pred. No. 8.2e-43;
Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSPOLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113

RESULT 7
US-10-726-332-215
; Sequence 215, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-215

Query Match          93.2%; Score 550; DB 5; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.9e-42;
Matches 106; Conservative 5; Mismatches 0; Indels 2; Gaps 1;

QY 1 DIVMTQSLPLVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSPOLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113

; Sequence 89, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-89

Query Match          93.9%; Score 554; DB 6; Length 113;
Best Local Similarity 93.8%; Pred. No. 8.2e-43;
Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSPOLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113

RESULT 8
US-11-021-715-88
; Sequence 88, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-88

Query Match          93.1%; Score 549; DB 6; Length 113;
Best Local Similarity 92.9%; Pred. No. 2.4e-42;
Matches 105; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSPOLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113

RESULT 9
US-10-309-762-165
; Sequence 165, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-165

Query Match          93.0%; Score 548.5; DB 4; Length 110;
Best Local Similarity 94.7%; Pred. No. 2.5e-42;
Matches 107; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 DIVMTQSLPLVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLVTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGSPOLLIYLSNRA 60
```

QY 61 SGVPRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 113  
|||||  
Db 61 SGVPRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 110  
|||||

## RESULT 10

US-11-021-715-74  
; Sequence 74, Application US/11021715  
; Publication No. US20050208596A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET  
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: 053893-5050  
; CURRENT APPLICATION NUMBER: US/11/021,715  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: PCT/US03/21304  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,352  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 60/411,694  
; PRIOR FILING DATE: 2002-09-18  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 74  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-715-74

Query Match 93.0%; Score 548.5; DB 6; Length 112;  
Best Local Similarity 94.7%; Pred. No. 2.6e-42; Indels 1; Gaps 1;  
Matches 107; Conservative 3; Mismatches 2;  
QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60  
|||||  
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60  
|||||  
QY 61 SGVPRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 113  
|||||  
Db 61 SGVPRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 112  
|||||

## RESULT 11

US-10-292-088-104  
; Sequence 104, Application US/10292088  
; Publication No. US2003021100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 104  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-088-104

Query Match 92.8%; Score 547.5; DB 4; Length 112;  
Best Local Similarity 94.7%; Pred. No. 3.2e-42; Indels 1; Gaps 1;  
Matches 107; Conservative 3; Mismatches 2;  
QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60  
|||||

Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60  
|||||  
QY 61 SGVPRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 113  
|||||  
Db 61 SGVPRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 112  
|||||

## RESULT 12

US-11-021-715-75  
; Sequence 75, Application US/11021715  
; Publication No. US20050208596A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET  
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: 053893-5050  
; CURRENT APPLICATION NUMBER: US/11/021,715  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: PCT/US03/21304  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,352  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 60/411,694  
; PRIOR FILING DATE: 2002-09-18  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 75  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-715-75

Query Match 92.8%; Score 547.5; DB 6; Length 112;  
Best Local Similarity 94.7%; Pred. No. 3.2e-42; Indels 1; Gaps 1;  
Matches 107; Conservative 3; Mismatches 2;  
QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60  
|||||  
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60  
|||||  
QY 61 SGVPRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 113  
|||||  
Db 61 SGVPRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 112  
|||||

## RESULT 13

US-11-021-715-92  
; Sequence 92, Application US/11021715  
; Publication No. US20050208596A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET  
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: 053893-5050  
; CURRENT APPLICATION NUMBER: US/11/021,715  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: PCT/US03/21304  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,352  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 60/411,694  
; PRIOR FILING DATE: 2002-09-18  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 92  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-715-92

Query Match 92.8%; Score 547.5; DB 6; Length 112;  
Best Local Similarity 92.9%; Pred. No. 3.2e-42;

Matches 105; Conservative 7; Mismatches 0; Indels 1; Gaps 1;

QY 1 DIVMTQSLPLPVTGEPASISCRSSQSLHNSGNYLDWYQKPGQSPQLLIYLGSNRA 60  
 |||||  
 Db 1 DIVMTQSLPLPVTGEPASISCRSSQSLHNSGNYLDWYQKPGQSPQLLIYLGSNRA 60  
 |||||

QY 61 SGVDFRFGSGSGTDTFTLKISRVEADVGVYVYCMQALQSLMCSFGQGTLEIK 113  
 |||||  
 Db 61 SGVDFRFGSGSGTDTFTLKISRVEADVGVYVYCMQALQTLI-TFGQGTLEIK 112  
 |||||

RESULT 14  
 US-10-834-397-15  
 ; Sequence 15, Application US/10834397  
 ; Publication No. US20060003334A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knappik, Achim  
 ; Pack, Peter  
 ; Ilag, Vic  
 ; Ge, Liming  
 ; Moroney, Simon  
 ; Plueckthun, Andreas  
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 ; NUMBER OF SEQUENCES: 373  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10021  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/834,397  
 ; FILING DATE: 29-Apr-2004  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/490,324  
 ; FILING DATE: 24-Jan-2000  
 ; APPLICATION NUMBER: US/09/025,769  
 ; FILING DATE: 18-FEB-1998  
 ; APPLICATION NUMBER: EP 95 11 3021.0  
 ; FILING DATE: 18-AUG-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: James F. Haley, Jr., Esq.  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: MORPHO/5  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212)596-9000  
 ; TELEFAX: (212)596-9090  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 113 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: <Unknown>  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 US-10-834-397-15

Query Match 92.8%; Score 547.5; DB 5; Length 113;  
 Best Local Similarity 94.7%; Pred. No. 3.2e-42;  
 Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSLPLPVTGEPASISCRSSQSLHNSGNYLDWYQKPGQSPQLLIYLGSNRA 60  
 |||||  
 Db 1 DIVMTQSLPLPVTGEPASISCRSSQSLHNSGNYLDWYQKPGQSPQLLIYLGSNRA 60  
 |||||

QY 61 SGVDFRFGSGSGTDTFTLKISRVEADVGVYVYCMQALQSLMCSFGQGTLEIK 113  
 |||||

Db 61 SGVDFRFGSGSGTDTFTLKISRVEADVGVYVYCMQALQT-PYTFQGTLEIK 112  
 |||||

RESULT 15  
 US-10-726-332-24  
 ; Sequence 24, Application US/10726332  
 ; Publication No. US20050058649A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gregory M. Landes  
 ; APPLICANT: Mary Haak-Frendscho  
 ; APPLICANT: Ling Chen  
 ; APPLICANT: Yen-Wah R. Lee  
 ; APPLICANT: Meina Liang  
 ; APPLICANT: Xiao-Feng  
 ; APPLICANT: Xiao-Chi Jia  
 ; APPLICANT: Mark R. Nocerini  
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: ABGENIX.072A  
 ; CURRENT APPLICATION NUMBER: US/10/726,332  
 ; CURRENT FILING DATE: 2003-12-02  
 ; PRIOR APPLICATION NUMBER: n/a  
 ; PRIOR FILING DATE:  
 ; NUMBER OF SEQ ID NOS: 222  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 24  
 ; LENGTH: 112  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-726-332-24

Query Match 92.7%; Score 547; DB 5; Length 112;  
 Best Local Similarity 92.9%; Pred. No. 3.5e-42;  
 Matches 105; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

QY 1 DIVMTQSLPLPVTGEPASISCRSSQSLHNSGNYLDWYQKPGQSPQLLIYLGSNRA 60  
 |||||  
 Db 1 DIVMTQSLPLPVTGEPASISCRSSQSLHNSGNYLDWYQKPGQSPQLLIYLGSNRA 60  
 |||||

QY 61 SGVDFRFGSGSGTDTFTLKISRVEADVGVYVYCMQALQSLMCSFGQGTLEIK 113  
 |||||  
 Db 61 SGVDFRFGSGSGTDTFTLKISRVEADVGVYVYCMQALQTI--TFQGTLEIK 111  
 |||||

Search completed: April 25, 2007, 04:22:50  
 Job time : 41.8164 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 04:23:02 ; Search time 44 Seconds  
(without alignments)  
533.620 Million cell updates/sec

Title: US-10-665-383-40

Perfect score: 590

Sequence: 1 DIVMTQSPSLPVTGEPAS.....MQALQSLMCSFGQGTKLEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 947558 seqs, 205760075 residues

Total number of hits satisfying chosen parameters: 947558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

Published Applications\_AA\_New\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/ECT\_NEW\_PUB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	113	7	US-11-109-181-30
2	590	100.0	113	7	US-11-109-181-221
3	590	100.0	113	7	US-11-109-181-255
4	576.5	97.7	114	7	US-11-109-181-322
5	554	93.9	114	7	US-11-428-895-19
6	554	93.9	131	7	US-11-428-895-25
7	550	93.2	111	7	US-11-433-924-268
8	550	93.2	223	7	US-11-396-178-98
9	550	93.2	223	7	US-11-396-178-156
10	548	92.8	112	7	US-11-428-895-20
11	547.5	92.6	112	7	US-11-211-917-104
12	546.5	92.6	112	7	US-11-256-332-128
13	546.5	92.6	112	7	US-11-369-641-4
14	546.5	92.6	113	7	US-11-256-332-118
15	546.5	92.6	113	7	US-11-311-939-639
16	546.5	92.6	115	7	US-11-256-332-73
17	546.5	92.6	115	7	US-11-256-332-81
18	546.5	92.6	115	7	US-11-256-332-89
19	546.5	92.6	115	7	US-11-256-332-97
20	546.5	92.6	134	7	US-11-303-478-8
21	546.5	92.6	134	7	US-11-303-478-8
22	545.5	92.5	112	7	US-11-311-164-8
23	544.5	92.3	111	7	US-11-311-939-646
24	544.5	92.3	112	7	US-11-239-308-16
25	544.5	92.3	112	7	US-11-211-917-103

#### ALIGNMENTS

##### RESULT 1

US-11-109-181-30  
; Sequence 30, Application US/11109181  
; Publication No. US20060293506A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Peng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Biyem  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: ABGENIX.051A  
; CURRENT APPLICATION NUMBER: US/11/109,181  
; CURRENT FILING DATE: 2005-04-18  
; PRIOR APPLICATION NUMBER: US/10/041,860  
; PRIOR FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-11-109-181-30

Query Match 100.0%; Score 590; DB 7; Length 113;  
Best Local Similarity 100.0%; Pred. No. 5e-48;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSGNYLDWYLRKPGQSPQLIYIGSNRA 60

DB 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSGNYLDWYLRKPGQSPQLIYIGSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEADGVYVYCNQALQSLMCSFGQGTKLEIK 113

DB 61 SGVPDRFSGSGGTDFTLKISRVEADGVYVYCNQALQSLMCSFGQGTKLEIK 113

##### RESULT 2

US-11-109-181-221  
; Sequence 221, Application US/11109181  
; Publication No. US20060293506A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi

```

; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX 051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 113
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-221

Query Match      100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 5e-48;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVTPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEADDGVYYCMQALQSLMCSFGGQTKLEIK 113
Db 61 SGVPDRFSGSGGTDFTLKISRVEADDGVYYCMQALQSLMCSFGGQTKLEIK 113

RESULT 3
US-11-109-181-255
; Sequence 255, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX 051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255
; LENGTH: 113
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-255

Query Match      100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 5e-48;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVTPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEADDGVYYCMQALQSLMCSFGGQTKLEIK 113
Db 61 SGVPDRFSGSGGTDFTLKISRVEADDGVYYCMQALQSLMCSFGGQTKLEIK 113
```

```

RESULT 4
US-11-109-181-322
; Sequence 322, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX 051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 322
; LENGTH: 114
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-322

Query Match      97.7%; Score 576.5; DB 7; Length 114;
Best Local Similarity 98.2%; Pred. No. 9.3e-47;
Matches 112; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVTPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEADDGVYYCMQALQSLMCSFGGQTKLEIK 113
Db 61 SGVPDRFSGSGGTDFTLKISRVEADDGVYYCMQALQSLMCSFGGQTKLEIK 114

RESULT 5
US-11-428-895-19
; Sequence 19, Application US/11428895
; Publication No. US20070003554A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
; FILE REFERENCE: 011.00231
; CURRENT APPLICATION NUMBER: US/11/428,895
; CURRENT FILING DATE: 2006-07-06
; PRIOR APPLICATION NUMBER: US/09/430,048
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/106,275
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-428-895-19

Query Match      93.9%; Score 554; DB 7; Length 114;
Best Local Similarity 93.8%; Pred. No. 1.2e-44;
Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVTPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
```



APPLICANT: JIA, Xiao-Chi  
APPLICANT: GUDAS, Jean  
TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT  
TITLE OF INVENTION: BIND TO 16P2F10B PROTEINS  
FILE REFERENCE: 511582006221  
CURRENT APPLICATION NUMBER: US/11/396,178  
CURRENT FILING DATE: 2006-03-31  
PRIOR APPLICATION NUMBER: 10/291,241  
PRIOR FILING DATE: 2002-11-07  
PRIOR APPLICATION NUMBER: 10/005,480  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: 60/667,588  
PRIOR FILING DATE: 2005-03-31  
PRIOR APPLICATION NUMBER: 60/700,975  
PRIOR FILING DATE: 2005-07-20  
NUMBER OF SEQ ID NOS: 177  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 156  
LENGTH: 223  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: 211  
OTHER INFORMATION: Xaa = Any amino acid.  
US-11-396-178-156

Query Match 93.2%; Score 550; DB 7; Length 223;  
Best Local Similarity 93.8%; Pred. No. 5.8e-44;  
Matches 106; Conservative 5; Mismatches 0; Indels 2; Gaps 1;

QY 1 DIVMTQSLPLVPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60  
DB 8 DIVMTQSLPLVPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 67  
QY 61 SGVPDRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 113  
DB 68 SGVPDRFSGSGGTDTLTKISRVEADDGVVYCMQALQTI--TFQGTKEIK 118

## RESULT 10

US-11-428-895-20  
Sequence 20, Application US/11428895  
Publication No. US20070003554A1  
GENERAL INFORMATION:  
APPLICANT: Miller, Jonathan L  
TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions  
TITLE OF INVENTION: of Antibodies to Human Platelet Glycoprotein Ib Alpha  
FILE REFERENCE: 011.00231  
CURRENT APPLICATION NUMBER: US/11/428,895  
CURRENT FILING DATE: 2006-07-06  
PRIOR APPLICATION NUMBER: US/09/430,048  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 60/106,275  
PRIOR FILING DATE: 1998-10-30  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 20  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-428-895-20

Query Match 92.9%; Score 548; DB 7; Length 112;  
Best Local Similarity 94.7%; Pred. No. 4.4e-44;  
Matches 107; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 1 DIVMTQSLPLVPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60  
DB 1 DIVMTQSLPLVPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60  
QY 61 SGVPDRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 113

DB 61 SGVPDRFSGSGGTDTLTKISRVEADDGVVYCMQALQTI--PTFGQGTKEIK 111

## RESULT 11

US-11-211-917-104  
Sequence 104, Application US/11211917  
Publication No. US20060093600A1  
GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40  
FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/11/211,917  
CURRENT FILING DATE: 2005-08-25  
PRIOR APPLICATION NUMBER: US/10/292,088  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 104  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-211-917-104

Query Match 92.8%; Score 547.5; DB 7; Length 112;  
Best Local Similarity 94.7%; Pred. No. 4.8e-44;  
Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSLPLVPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60  
DB 1 DIVMTQSLPLVPTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60  
QY 61 SGVPDRFSGSGGTDTLTKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 113  
DB 61 SGVPDRFSGSGGTDTLTKISRVEADDGVVYCMQALQTI--PYTFQGTKEIK 112

## RESULT 12

US-11-256-332-128  
Sequence 128, Application US/11256332  
Publication No. US20060228349A1  
GENERAL INFORMATION:  
APPLICANT: Acton, Paul  
APPLICANT: An, Zhidong  
APPLICANT: Bett, Andrew J.  
APPLICANT: Breese, Robert  
APPLICANT: Chen Dodson, Elizabeth  
APPLICANT: Kinney, Gene  
APPLICANT: Klein, William R.  
APPLICANT: Kraft, Grant A.  
APPLICANT: Lambert, Mary P.  
APPLICANT: Liang, Xiaoping  
APPLICANT: Pray, Todd R.  
APPLICANT: Shughrue, Paul  
APPLICANT: Strohl, William R.  
APPLICANT: Wang, Fubao  
TITLE OF INVENTION: ANTI-ADDL ANTIBODIES AND USES THEREOF  
FILE REFERENCE: MRK0002US  
CURRENT APPLICATION NUMBER: US/11/256,332  
CURRENT FILING DATE: 2005-10-21  
PRIOR APPLICATION NUMBER: US 60/621,776  
PRIOR FILING DATE: 2004-10-25  
PRIOR APPLICATION NUMBER: US 60/652,538  
PRIOR FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: US 60/695,528  
PRIOR FILING DATE: 2005-06-30  
PRIOR APPLICATION NUMBER: US 60/695,526  
PRIOR FILING DATE: 2005-06-30



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; NUMBER OF SEQ ID NOS: 322
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-256-332-128

Query Match      92.6%; Score 546.5; DB 7; Length 112;
Best Local Similarity 93.8%; Pred. No. 6e-44;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DVVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113
Db 61 SGVPDRFSGSGGTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 112

RESULT 13
US-11-369-641-4
; Sequence 4, Application US/11369641
; Publication No. US20060258852A1
; GENERAL INFORMATION:
; APPLICANT: Lugovskoy, Alexey Alexandrovich et al.
; TITLE OF INVENTION: METHODS OF HUMANIZING IMMUNOGLOBULIN VARIABLE REGIONS
; TITLE OF INVENTION: THROUGH RATIONAL MODIFICATION OF COMPLEMENTARITY
; FILE REFERENCE: BGN-A230
; CURRENT APPLICATION NUMBER: US/11/369,641
; CURRENT FILING DATE: 2006-03-06
; PRIOR APPLICATION NUMBER: 60/658,987
; PRIOR FILING DATE: 2005-03-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; TYPE: PRT
; LENGTH: 112
; ORGANISM: Homo sapiens
US-11-369-641-4

Query Match      92.6%; Score 546.5; DB 7; Length 112;
Best Local Similarity 93.8%; Pred. No. 6e-44;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DVVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113
Db 61 SGVPDRFSGSGGTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 112

RESULT 14
US-11-256-332-118
; Sequence 118, Application US/11256332
; Publication No. US20060228349A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Paul
; APPLICANT: An, Zhiqiang
; APPLICANT: Bett, Andrew J.
; APPLICANT: Breese, Robert
; APPLICANT: Chen Dodson, Elizabeth
; APPLICANT: Kinney, Gene
; APPLICANT: Klein, William R.
; APPLICANT: Kraft, Grant A.
; APPLICANT: Lambert, Mary P.
; APPLICANT: Liang, Xiaoping
; APPLICANT: Pray, Todd R.
; APPLICANT: Shughrue, Paul

; APPLICANT: Scrohl, William R.
; APPLICANT: Wang, Fubao
; TITLE OF INVENTION: ANTI-ADDL ANTIBODIES AND USES THEREOF
; FILE REFERENCE: MRK0002US
; CURRENT APPLICATION NUMBER: US/11/256,332
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: US 60/621,776
; PRIOR FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: US 60/652,538
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/695,528
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US 60/695,526
; PRIOR FILING DATE: 2005-06-30
; NUMBER OF SEQ ID NOS: 322
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 118
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-256-332-118

Query Match      92.6%; Score 546.5; DB 7; Length 113;
Best Local Similarity 93.8%; Pred. No. 6.1e-44;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DVVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113
Db 61 SGVPDRFSGSGGTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 112

RESULT 15
US-11-311-939-639
; Sequence 639, Application US/11311939
; Publication No. US20060246071A1
; GENERAL INFORMATION:
; APPLICANT: Green, Larry L.
; APPLICANT: Zhou, Qing
; APPLICANT: Keyt, Bruce A.
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Emery, Stephen
; APPLICANT: Blakey, David C.
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO ANGIOPOIETIN-2
; FILE REFERENCE: ABXAZ.002A
; CURRENT APPLICATION NUMBER: US/11/311,939
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: US 60/638,354
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/711,289
; PRIOR FILING DATE: 2005-08-25
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-311-939-639

Query Match      92.6%; Score 546.5; DB 7; Length 113;
Best Local Similarity 93.8%; Pred. No. 6.1e-44;
Matches 106; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DVVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113
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Db 61 SGVDRFSGSGTDTTLKISRVEADVGVYCMQALOTPI-TFGQTRLEIK 112

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Job time : 43.572 secs